

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property

Organization

International Bureau

(43) International Publication Date

18 June 2020 (18.06.2020)



(10) International Publication Number

WO 2020/123286 A1

(51) International Patent Classification:

A61K 31/122 (2006.01) A61K 9/00 (2006.01)

A61K 38/51 (2006.01)

(21) International Application Number:

PCT/US2019/064891

(22) International Filing Date:

06 December 2019 (06.12.2019)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

62/779,647 14 December 2018 (14.12.2018) US

(71) Applicant: CODEXIS, INC. [US/US]; 200 Penobscot Drive, Redwood City, California 94063 (US).

(72) Inventors: LIU, Joyce; 200 Penobscot Drive, Redwood City, California 94063 (US). DELLAS, Nikki; 200 Penobscot Drive, Redwood City, California 94063 (US). JENNE, Stephan; 200 Penobscot Drive, Redwood City, California 94063 (US).

(74) Agent: MACKNIGHT, Kamrin, T. et al.; Codexis, Inc., 200 Penobscot Drive, Redwood City, California 94063 (US).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

(54) Title: ENGINEERED TYROSINE AMMONIA LYASE

(57) Abstract: The present invention provides engineered tyrosine ammonia-lyase (TAL) polypeptides and compositions thereof. In some embodiments, the engineered TAL polypeptides have been optimized to provide enhanced catalytic activity while reducing sensitivity to proteolysis and increasing tolerance to acidic pH levels. The invention also provides methods for utilization of the compositions comprising the engineered TAL polypeptides for therapeutic and industrial purposes.



WO 2020/123286 A1

ENGINEERED TYROSINE AMMONIA LYASE

[0001] The present application claims priority to US Prov. Appln. Ser. No. 62/779,647, filed December 14, 2018, hereby incorporated by reference in its entirety for all purposes.

REFERENCE TO A "SEQUENCE LISTING," A TABLE, OR A COMPUTER PROGRAM LISTING APPENDIX SUBMITTED AS AN ASCII TEXT FILE

[0002] The Sequence Listing written in file CX7-182WO2_ST25.TXT, created on December 14, 2018, size of 7.80 MB, machine format IBM-PC, MS-Windows operating system, is hereby incorporated by reference.

FIELD OF THE INVENTION

[0003] The present invention provides engineered tyrosine ammonia-lyase (TAL) polypeptides and compositions thereof. In some embodiments, the engineered TAL polypeptides have been optimized to provide enhanced catalytic activity while reducing sensitivity to proteolysis and increasing tolerance to acidic pH levels. The invention also provides methods for utilization of the compositions comprising the engineered TAL polypeptides for therapeutic and industrial purposes.

BACKGROUND OF THE INVENTION

[0004] Tyrosine ammonia lyase (TAL; also referred to as tyrase, L-tyrosine ammonia lyase, and "L-tyrosine ammonia lyase [trans-p-hydroxycinnamate forming]"), along with histidine ammonia lyase (HAL) and phenylalanine ammonia-lyase (PAL) are members of the aromatic amino acid lyase family (EC 4.3.1.23-1.25 and 4.3.1.3). The enzymes having TAL activity are currently classified in EC4.3.1.23 (previously classified as EC 4.3.1.5). TAL catalyzes the formation of p-coumaric acid from L-tyrosine.

[0005] Tyrosinemia (also referred to as "hereditary tyrosinemia," and "hypertyrosinemia") is a genetic disorder characterized by elevated blood levels of tyrosine, due to the deficiency of an enzyme required for the catabolism of tyrosine in the liver. If untreated, tyrosine and other metabolites accumulate in the tissues and organs of affected individuals, resulting in serious medical issues. Tyrosinemia is an inborn error of metabolism inherited in an autosomal recessive pattern. There are three types of tyrosinemia, each caused by the deficiency of a different enzyme. Currently used treatment methods depend upon the type of tyrosinemia involved. A low protein diet is often used.

[0006] Type I tyrosinemia (also referred to as "FAH deficiency," "fumaryl acetoacetase deficiency," "fumaryl acetoacetate hydrolase deficiency," "hereditary infantile tyrosinemia," and "hepatorenal tyrosinemia") is caused by a deficiency of fumarylacetoacetate hydrolase, due to mutations in the *fah* gene. This is the most severe form of the disease, with symptoms usually appearing in the first few months of life, commonly including failure to thrive, diarrhea, bloody stools, vomiting, jaundice,

enlarged liver, the tendency to easily bruise, lethargy, irritability, fever, and other symptoms, such as a distinctive cabbage-like odor of the skin and urine. Some affected infants have repeated neurologic episodes of acute polyneuropathy, characterized by severe leg pain, as well as altered mental status, abdominal pain, and respiratory failure. Infants with the acute form are typically affected at birth and there is a rapid onset of symptoms that can lead to developmental delays, enlarged spleen, ascites, kidney disease, and blood clotting abnormalities. Untreated, it can lead to hepatic and renal failure, nervous system problems, and an increased risk of liver cancer (e.g., hepatocellular carcinoma). In some cases, hypertension and hypertrophic cardiomyopathy are present. If untreated, this disease can be fatal. In the less-common chronic form, the symptoms exhibit a more gradual onset and tend to be less severe. Affected infants initially exhibit vomiting, diarrhea, enlarged liver and spleen, and failure to thrive. Eventually, progressive liver cirrhosis occurs, leading to chronic liver failure, developmental delays, and renal Fanconi syndrome (a rare kidney disorder characterized by weakening and softening of the bones [rickets], vomiting, dehydration, weakness, and fever). In some cases, the most effective treatment has been full or partial liver transplant. Worldwide, this form affects approximately 1 in 100,000 human births (Genetics Home Reference, U.S. National Library of Medicine).

[0007] Type II tyrosinemia (also referred to as “keratosis palmoplantaris-corneal dystrophy,” oculocutaneous tyrosinemia,” “Richner-Hanhart syndrome,” “tyrosinemia due to TAT deficiency,” and “tyrosinemia due to tyrosine aminotransferase deficiency,”) is caused by a deficiency of tyrosine aminotransferase, due to mutations in the *tat* gene. It affects the eyes, skin, and mental development. As with Type I tyrosinemia, symptoms usually begin in early life, and include excessive tearing, photophobia, eye pain and redness, and painful skin lesions on the palms and soles. About half of affected individuals have some level of intellectual disability. This form occurs in less than 1 in 250,000 persons (Genetics Home Reference, *supra*).

[0008] Type III tyrosinemia (also referred to as “tyrosinemia due to 4-hydroxyphenylpyruvate dioxygenase deficiency,” “tyrosinemia due to 4-hydroxyphenylpyruvate acid oxidase deficiency,” and “tyrosinemia due to HPD deficiency”) is a rare disorder, caused by a deficiency of 4-hydroxyphenylpyruvate dioxygenase, due to mutations in the *hpd* gene. Symptoms of this form include intellectual disability, seizures, and intermittent ataxia. This form is very rare, only a few cases have been reported (Genetics Home Reference, *supra*).

[0009] There are additional cases in which there are temporary elevated tyrosine levels, due to non-genetic factors such as vitamin C deficiency or premature birth, which results in immature liver enzymes. Differential diagnoses are used to differentiate these transient cases from tyrosinemia I, II, or III.

[0010] In addition to tyrosinemia, there are other diseases associated with insufficient or absent tyrosine metabolism. For example, alkaptonuria also referred to as alcaptonuria, is a disease caused by deficiency of homogentisate 1,2-dioxygenase, which is an enzyme involved in tyrosine

degradation. This enzyme is encoded by the *HGD* gene. Insufficient activity of this enzyme results in the accumulation of homogentisic acid. Excess homogentisic acid and related compounds are deposited in connective tissues, causing the cartilage and skin to darken. Over time, arthritis may result due to the accumulation of homogentisic acid and related metabolites in the joints of affected individuals. Homogentisic acid is also excreted in urine, making the urine turn black. Alkaptonuria is a rare disease that affects 1 in 250,000 to 1,000,000 people worldwide (See, Genetics Home Reference, *supra*).

[0011] Treatment of these diseases has largely been the life-long use of a phenylalanine-, and tyrosine-restricted diet. Treatment with nitisinone (NTBC; 2-(2-nitro-4-trifluoromethylbenzol)-1,3-cyclohexane dione; Orfadin®) has been reported to be helpful for type I tyrosinemia and alkaptonuria, due to its inhibition of the 4-hydroxyphenylpyruvate oxidase pathway. However, NTBC must be used in combination with a challenging and costly phenylalanine-, and tyrosine-restricted diet to prevent both liver failure and carcinogenesis. There remains a need in the art for easy to administer, effective treatment(s) to ameliorate the symptoms of these diseases and allow patients to utilize normal diets.

SUMMARY OF THE INVENTION

[0012] The present invention provides engineered tyrosine ammonia-lyase (TAL) polypeptides and compositions thereof. In some embodiments, the engineered TAL polypeptides have been optimized to provide enhanced catalytic activity while reducing sensitivity to proteolysis and increasing tolerance to acidic pH levels. The invention also provides methods for utilization of the compositions comprising the engineered TAL polypeptides for therapeutic and industrial purposes.

[0013] In some embodiments, the present invention provides engineered TAL polypeptides (also referred to herein as “recombinant TAL polypeptides”) and biologically active fragments and analogs thereof having improved properties when compared to a wild-type TAL enzyme and/or a reference TAL polypeptide under essentially the same conditions. The invention is further directed to methods of using the engineered TAL polypeptides and biologically active fragments and analogs thereof in therapeutic and/or industrial compositions.

[0014] The present invention provides recombinant tyrosine ammonia lyases and/or biologically active recombinant tyrosine ammonia lyase fragments comprising an amino acid sequence comprising at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 2. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution at position or set of positions selected from 79/95/107, 79/107, 79/107/410, 79/410, 95/107/184, 95/107/184/534, 95/184/534, 99/107/184, 107/184/534, and 107/401/534, wherein the positions are numbered with reference to SEQ ID NO: 2. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets at one or more positions selected from 79T/95A/107S, 79T/107S, 79T/107S/410K, 79T/410K, 95A/107A/184S,

95A/107S/184S/534S, 95A/184S/534S, 99H/107A/184S, 107A/184S/534S, and 107S/401P/534S, wherein the positions are numbered with reference to SEQ ID NO: 2. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets at one or more positions selected from S79T/K95A/V107S, S79T/V107S, S79T/V107S/P410K, S79T/P410K, K95A/V107A/Y184S, K95A/V107S/Y184S/A534S, K95A/Y184S/A534S, N99H/V107A/Y184S, V107A/Y184S/A534S, and V107S/A401P/A534S, wherein the positions are numbered with reference to SEQ ID NO: 2.

[0015] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 28, 29, 33, 33/34/37/46/279/554, 33/34/37/90/554, 33/34/46/66/90/289, 33/34/90/289/554, 33/34/279/289, 33/66, 33/66/289, 33/66/289/554, 34/37/46/289, 34/37/66/279/289, 34/46, 34/56/90, 34/56/90/289, 34/66/289, 34/90/289/554, 34/90/519, 36/70/234/302/461/500, 36/79, 36/79/304/407, 36/79/407/461/500/531, 36/111/304/461/531, 36/407/461/500/531, 37, 46, 46/66/289/519/554, 49, 56, 66, 66/90/279/289/554, 66/90/289/554, 69, 70/79/234/361/407, 70/111/461/500/531, 70/304/407/461, 72, 79/111/234/361/500, 79/111/234/531, 79/111/361, 79/111/531, 79/304/361, 79/304/461/531, 79/407/461, 88, 90/289/519, 90/289/554, 131, 142, 198, 201, 272, 278, 279/289/554, 289/519/554, 289/554, 295, 304/361, 305, 350, 361/500/531, 461/500, 490, 491, 499, 510, 518, 519, 521, 522, 523, 524, 531, 540, 541, 544, 547, 548, 554, 557, 558, and 560, wherein the positions are numbered with reference to SEQ ID NO: 14. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 28A, 28C, 28G, 28N, 28T, 29A, 29E, 29G, 29R, 29W, 33D/34E/37S/46R/279S/554Q, 33D/34E/37S/90S/554Q, 33D/34E/46R/66N/90S/289R, 33D/34E/90S/289R/554Q, 33D/34E/279S/289R, 33D/66N, 33D/66N/289R, 33D/66N/289R/554Q, 33N, 34E/37R/46R/289R, 34E/37S/66N/279S/289R, 34E/46R, 34E/56G/90S, 34E/56G/90S/289R, 34E/66N/289R, 34E/90S/289R/554Q, 34E/90S/519P, 36V/70K/234H/302M/461M/500T, 36V/79T, 36V/79T/304G/407V, 36V/79T/407V/461M/500T/531D, 36V/111K/304G/461M/531D, 36V/407V/461M/500T/531D, 37A, 37D, 46R, 46R/66N/289R/519P/554Q, 46T, 49D, 49N, 56G, 56R, 66N/90S/279D/289R/554Q, 66N/90S/289R/554Q, 66R, 66S, 69S, 70K/79T/234H/361M/407V, 70K/111K/461M/500T/531D, 70K/304G/407V/461M, 72T, 79T/111K/234H/361M/500T, 79T/111K/234H/531D, 79T/111K/361M, 79T/111K/531D, 79T/304G/361M, 79T/304G/461M/531D, 79T/407V/461M, 88E, 88Q, 90S/289R/519P, 90S/289R/554Q, 131G, 131M, 131S, 131W, 142R, 198R, 201R, 272S, 278S, 279S/289R/554Q, 289R/519P/554Q, 289R/554Q, 295Q, 304G/361M, 305H, 350G, 361M/500Q/531D, 461M/500T, 490A, 490I, 490S, 490V, 491L, 491V, 499T, 510K, 518E, 518V, 519D, 519E, 519L, 519P, 519Q, 521D, 522G, 522K, 522R, 522V, 522Y, 523A, 523D, 523H, 523I, 523S, 524A, 524I, 524L, 524Q, 524T, 524Y, 531D, 540E, 540R, 541A, 544E, 544G, 544R, 544S, 547A, 547C, 547G, 547K, 547Q, 547R, 547S, 548A, 548G, 548K, 548Q, 548R, 548T, 554E, 554R, 554S, 554Y, 557E, 557R, 558A, 558D, 558H, 558S, 560G, 560M, 560R, and 560T, wherein the positions are numbered with reference to SEQ ID NO: 14. In some embodiments, the

tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from K28A, K28C, K28G, K28N, K28T, P29A, P29E, P29G, P29R, P29W, K33D/K34E/Q37S/L46R/Q279S/K554Q, K33D/K34E/Q37S/T90S/K554Q, K33D/K34E/L46R/Q66N/T90S/A289R, K33D/K34E/T90S/A289R/K554Q, K33D/K34E/Q279S/A289R, K33D/Q66N, K33D/Q66N/A289R, K33D/Q66N/A289R/K554Q, K33N, K34E/Q37R/L46R/A289R, K34E/Q37S/Q66N/Q279S/A289R, K34E/L46R, K34E/K56G/T90S, K34E/K56G/T90S/A289R, K34E/Q66N/A289R, K34E/T90S/A289R/K554Q, K34E/T90S/A519P, A36V/S70K/Y234H/R302M/L461M/C500T, A36V/S79T, A36V/S79T/E304G/S407V, A36V/S79T/S407V/L461M/C500T/N531D, A36V/Q111K/E304G/L461M/N531D, A36V/S407V/L461M/C500T/N531D, Q37A, Q37D, L46R, L46R/Q66N/A289R/A519P/K554Q, L46T, T49D, T49N, K56G, K56R, Q66N/T90S/Q279D/A289R/K554Q, Q66N/T90S/A289R/K554Q, Q66R, Q66S, A69S, S70K/S79T/Y234H/L361M/S407V, S70K/Q111K/L461M/C500T/N531D, S70K/E304G/S407V/L461M, E72T, S79T/Q111K/Y234H/L361M/C500T, S79T/Q111K/Y234H/N531D, S79T/Q111K/L361M, S79T/Q111K/N531D, S79T/E304G/L361M, S79T/E304G/L461M/N531D, S79T/S407V/L461M, V88E, V88Q, T90S/A289R/A519P, T90S/A289R/K554Q, H131G, H131M, H131S, H131W, Q142R, E198R, K201R, P272S, A278S, Q279S/A289R/K554Q, A289R/A519P/K554Q, A289R/K554Q, L295Q, E304G/L361M, Q305H, A350G, L361M/C500Q/N531D, L461M/C500T, K490A, K490I, K490S, K490V, I491L, I491V, Q499T, L510K, K518E, K518V, A519D, A519E, A519L, A519P, A519Q, S521D, E522G, E522K, E522R, E522V, E522Y, E523A, E523D, E523H, E523I, E523S, R524A, R524I, R524L, R524Q, R524T, R524Y, N531D, A540E, A540R, L541A, A544E, A544G, A544R, A544S, T547A, T547C, T547G, T547K, T547Q, T547R, T547S, S548A, S548G, S548K, S548Q, S548R, S548T, K554E, K554R, K554S, K554Y, N557E, N557R, Q558A, Q558D, Q558H, Q558S, V560G, V560M, V560R, and V560T, wherein the positions are numbered with reference to SEQ ID NO: 14.

[0016] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 28/34/49/70/234/289/544/554, 33/34/49/234/531/547/554, 33/34/66/70/519/531, 33/34/66/289/522/531, 33/34/70/234/289/519, 33/34/70/234/518/519/547/554, 33/34/70/289/522/554, 33/34/289/522/531, 34/49/66/531, 34/49/234/531/554, 34/49/289/544/547, 34/66/70/234/518/519/547, 34/66/531/554, 34/66/554, 34/70/234/289/522, 34/70/234/554, 34/70/289/522, 34/234/522/554, 34/289, 34/289/522/531, 34/289/522/544/554, 34/522, 34/544, 66/70/234, and 234/531/544/547, wherein the positions are numbered with reference to SEQ ID NO: 86. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 28/34/49/70/234/289/544/554, 33/34/49/234/531/547/554, 33/34/66/70/519/531, 33/34/66/289/522/531, 33/34/70/234/289/519, 33/34/70/234/518/519/547/554, 33/34/70/289/522/554, 33/34/289/522/531, 34/49/66/531, 34/49/234/531/554, 34/49/289/544/547, 34/66/70/234/518/519/547, 34/66/531/554, 34/66/554, 34/70/234/289/522, 34/70/234/554, 34/70/289/522, 34/234/522/554, 34/289, 34/289/522/531,

34/289/522/544/554, 34/522, 34/544, 66/70/234, and 234/531/544/547, wherein the positions are numbered with reference to SEQ ID NO: 86. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from

28N/34E/49N/70S/234Y/289R/544E/554Q, 33D/34E/66N/70S/519P/531D, 33D/34E/66N/289R/522K/531D, 33D/34E/70S/234Y/289R/519P, 33D/34E/70S/234Y/518V/519P/547Q/554Q, 33D/34E/70S/289R/522K/554Q, 33D/34E/289R/522K/531D, 33N/34E/49N/234Y/531D/547Q/554Q, 34E/49N/66N/531D, 34E/49N/234Y/531D/554Q, 34E/49N/289R/544E/547Q, 34E/66N/70S/234Y/518V/519P/547Q, 34E/66N/531D/554Q, 34E/66N/554Q, 34E/70S/234Y/289R/522K, 34E/70S/234Y/554Q, 34E/70S/289R/522K, 34E/234Y/522K/554Q, 34E/289R, 34E/289R/522K/531D, 34E/289R/522K/544E/554Q, 34E/522K, 34E/544E, 66N/70S/234Y, and 234Y/531D/544E/547Q, wherein the positions are numbered with reference to SEQ ID NO: 86.

[0017] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 31, 37/49/56/66/111, 37/49/56/234/557, 37/49/56/500/524, 37/49/66/111/234, 37/49/111/524, 37/111, 37/111/361/500/557/558, 37/234, 43/59/93/506, 43/306, 43/306/506, 49/56/66/111/153/234/500/524, 49/66, 56/111/234, 56/234/500, 61, 65, 65/336, 66, 66/111/234/500, 93/506, 95, 103, 103/107/417/421, 103/306/506, 103/421, 104/105, 107, 107/417/421, 111/234/548/558, 111/361, 145, 146, 155, 172, 197, 211, 234, 234/524, 237/238/506, 286, 304, 306, 306/506, 328, 336, 361/524/557/558, 407, 417/421, 421, 471, 504, 506, 549, and 558, wherein the positions are numbered with reference to SEQ ID NO: 334. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 31S, 37D/49N/56G/66N/111K, 37D/49N/56G/234Y/557E, 37D/49N/56G/500T/524Q, 37D/49N/66N/111K/234Y, 37D/49N/111K/524Q, 37D/111K, 37D/111K/361L/500T/557E/558D, 37D/234Y, 43T/59A/93Q/506R, 43T/306L, 43T/306L/506R, 49N/56G/66N/111K/153N/234Y/500T/524Q, 49N/66N, 56G/111K/234Y, 56G/234Y/500T, 61V, 65M, 65N/336V, 66N, 66N/111K/234Y/500T, 93Q/506R, 95K, 95V, 103L, 103W, 103W/107T/417A/421S, 103W/306L/506R, 103W/421S, 104F/105M, 107T, 107T/417A/421A, 111K/234Y/548K/558D, 111K/361L, 145V, 146K, 155L, 155S, 172S, 197T, 211K, 234Y, 234Y/524Q, 237R/238V/506R, 286Q, 286R, 304N, 306L, 306L/506R, 328A, 336V, 361L/524Q/557E/558D, 407K, 407T, 417A/421S, 421S, 471Y, 504R, 506R, 506V, 549D, and 558D, wherein the positions are numbered with reference to SEQ ID NO: 334. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from T31S, Q37D/T49N/K56G/Q66N/Q111K, Q37D/T49N/K56G/H234Y/N557E, Q37D/T49N/K56G/C500T/R524Q, Q37D/T49N/Q66N/Q111K/H234Y, Q37D/T49N/Q111K/R524Q, Q37D/Q111K, Q37D/Q111K/M361L/C500T/N557E/Q558D, Q37D/H234Y, A43T/S59A/L93Q/L506R, A43T/P306L, A43T/P306L/L506R, T49N/K56G/Q66N/Q111K/T153N/H234Y/C500T/R524Q,

T49N/Q66N, K56G/Q111K/H234Y, K56G/H234Y/C500T, C61V, A65M, A65N/I336V, Q66N, Q66N/Q111K/H234Y/C500T, L93Q/L506R, A95K, A95V, R103L, R103W, R103W/A107T/G417A/T421S, R103W/P306L/L506R, R103W/T421S, Y104F/H105M, A107T, A107T/G417A/T421A, Q111K/H234Y/S548K/Q558D, Q111K/M361L, E145V, T146K, H155L, H155S, A172S, P197T, L211K, H234Y, H234Y/R524Q, Q237R/N238V/L506R, A286Q, A286R, E304N, P306L, P306L/L506R, S328A, I336V, M361L/R524Q/N557E/Q558D, V407K, V407T, G417A/T421S, T421S, Q471Y, A504R, L506R, L506V, G549D, and Q558D, wherein the positions are numbered with reference to SEQ ID NO: 334.

[0018] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 31/61/95/286/328, 31/61/95/407/504, 31/61/95/471/504, 31/61/407/504, 31/95/155/286/504/549, 31/95/237/504/547/549, 31/95/286/504, 31/95/286/504/549, 31/95/328/504, 31/95/504, 31/95/549, 37/49/56/59/145, 37/103/111/145/421/500/524, 49/56/59/234/500, 49/59/66/111/145/234, 49/59/145/234/421, 56/59/66/234, 56/59/111/145, 56/59/111/145/234/421, 56/66/145/500, 56/103/111/145/234/500, 59/103/145/234/421/500, 59/103/234/421, 59/145, 59/234, 61, 61/95/155/286/407/471, 61/95/155/407, 61/95/286, 61/95/286/328/504, 61/95/328/407, 61/95/328/549, 61/95/407, 61/95/504/547, 61/286/407, 61/328, 61/328/504, 61/328/504/549, 61/407, 61/504, 66/103/145/234/421, 95/155/286/328/407/504, 95/155/286/549, 95/286, 95/286/328/407/504, 95/286/328/504, 95/286/547, 95/287/504/549, 95/328/504, 95/407, 95/407/504, 95/504/547, 95/549, 103/111/145/234/421, 111/145/234, 111/234, 145/234/500, 286/328/407/504/549, and 549, wherein the positions are numbered with reference to SEQ ID NO: 388. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 31S/61V/95K/286Q/328A, 31S/61V/95K/407T/504R, 31S/61V/95K/471Y/504R, 31S/61V/407T/504R, 31S/95K/155S/286Q/504R/549D, 31S/95K/237K/504R/547Q/549D, 31S/95K/286Q/504R, 31S/95K/286Q/504R/549D, 31S/95K/328A/504R, 31S/95K/504R, 31S/95K/549D, 37D/49N/56G/59A/145V, 37D/103L/111K/145V/421S/500T/524Q, 49N/56G/59A/234Y/500T, 49N/59A/66N/111K/145V/234Y, 49N/59A/145V/234Y/421S, 56G/59A/66N/234Y, 56G/59A/111K/145V, 56G/59A/111K/145V/234Y/421S, 56G/66N/145V/500T, 56G/103L/111K/145V/234Y/500T, 59A/103L/145V/234Y/421S/500T, 59A/103L/234Y/421S, 59A/145V, 59A/234Y, 61V, 61V/95K/155S/286Q/407T/471Y, 61V/95K/155S/407T, 61V/95K/286Q, 61V/95K/286Q/328A/504R, 61V/95K/328A/407T, 61V/95K/328A/549D, 61V/95K/407T, 61V/95K/504R/547Q, 61V/286Q/407T, 61V/328A, 61V/328A/504R, 61V/328A/504R/549D, 61V/407T, 61V/504R, 66N/103L/145V/234Y/421S, 95K/155S/286Q/328A/407T/504R, 95K/155S/286Q/549D, 95K/286Q, 95K/286Q/328A/407T/504R, 95K/286Q/328A/504R, 95K/286Q/547Q, 95K/287S/504R/549D, 95K/328A/504R, 95K/407T, 95K/407T/504R, 95K/504R/547Q, 95K/549D, 103L/111K/145V/234Y/421S, 111K/145V/234Y, 111K/234Y, 145V/234Y/500T, 286Q/328A/407T/504R/549D, and 549D, wherein the positions are numbered with

reference to SEQ ID NO: 388. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from T31S/C61V/A95K/A286Q/S328A, T31S/C61V/A95K/V407T/A504R, T31S/C61V/A95K/Q471Y/A504R, T31S/C61V/V407T/A504R, T31S/A95K/H155S/A286Q/A504R/G549D, T31S/A95K/Q237K/A504R/T547Q/G549D, T31S/A95K/A286Q/A504R, T31S/A95K/A286Q/A504R/G549D, T31S/A95K/S328A/A504R, T31S/A95K/A504R, T31S/A95K/G549D, Q37D/T49N/K56G/S59A/E145V, Q37D/R103L/Q111K/E145V/T421S/C500T/R524Q, T49N/K56G/S59A/H234Y/C500T, T49N/S59A/Q66N/Q111K/E145V/H234Y, T49N/S59A/E145V/H234Y/T421S, K56G/S59A/Q66N/H234Y, K56G/S59A/Q111K/E145V, K56G/S59A/Q111K/E145V/H234Y/T421S, K56G/Q66N/E145V/C500T, K56G/R103L/Q111K/E145V/H234Y/C500T, S59A/R103L/E145V/H234Y/T421S/C500T, S59A/R103L/H234Y/T421S, S59A/E145V, S59A/H234Y, C61V, C61V/A95K/H155S/A286Q/V407T/Q471Y, C61V/A95K/H155S/V407T, C61V/A95K/A286Q, C61V/A95K/A286Q/S328A/A504R, C61V/A95K/S328A/V407T, C61V/A95K/S328A/G549D, C61V/A95K/V407T, C61V/A95K/A504R/T547Q, C61V/A286Q/V407T, C61V/S328A, C61V/S328A/A504R, C61V/S328A/A504R/G549D, C61V/V407T, C61V/A504R, Q66N/R103L/E145V/H234Y/T421S, A95K/H155S/A286Q/S328A/V407T/A504R, A95K/H155S/A286Q/G549D, A95K/A286Q, A95K/A286Q/S328A/V407T/A504R, A95K/A286Q/S328A/A504R, A95K/A286Q/T547Q, A95K/G287S/A504R/G549D, A95K/S328A/A504R, A95K/V407T, A95K/V407T/A504R, A95K/A504R/T547Q, A95K/G549D, R103L/Q111K/E145V/H234Y/T421S, Q111K/E145V/H234Y, Q111K/H234Y, E145V/H234Y/C500T, A286Q/S328A/V407T/A504R/G549D, and G549D, wherein the positions are numbered with reference to SEQ ID NO: 388.

[0019] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 14/56/114, 14/114/283/289, 14/114/283/289/291, 14/114/283/289/562, 14/114/291/518/562, 14/114/518, 14/234/283/291/305, 14/283/289/562, 29/66/111, 29/66/111/540, 29/111, 29/111/523, 33/46/49, 33/46/49/336/519/548/549, 33/46/49/549, 33/46/518/534/548/549, 33/46/519, 33/49/336, 33/336/519, 36/37/56/59/145/234/328, 36/37/59/131/531, 36/37/103/234, 36/37/131/145/234/328, 36/37/145/234, 36/37/145/234/328/471/531, 36/37/234/328/531, 36/56/145/234/328, 36/59/234/328, 36/59/531, 36/103/145/328/531, 36/131, 36/234/531, 37/56/59/103/145/234/328/471/531, 37/56/59/234/328/524/531, 37/56/59/234/531, 37/56/234/531, 37/59/234, 37/234/471, 46/49, 46/49/518/519/548/549, 46/49/519, 46/155, 46/548, 49/519, 56, 56/59/103/471/531, 56/59/471/531, 56/114/206/283, 56/114/291, 56/114/291/518/562, 56/114/518, 56/518, 59/328/524/531, 66/540, 111, 111/510/521/523/541/558, 111/523/557, 114, 114/206/283/289/562, 114/283/289/291, 114/283/289/305/518, 114/283/291, 114/289, 114/289/562, 114/291, 114/291/518, 114/518/562, 114/562, 131/234/328, 234, 234/328, 234/328/471, 234/531, 289/562, 305, 336/519, 518/519/548/549, 519, 521, 523, 531, 541, 548/549, and 549, wherein the positions are numbered

with reference to SEQ ID NO: 604. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 14S/56R/114P, 14S/114P/283D/289Q, 14S/114P/283D/289Q/291V, 14S/114P/283S/289Q/562S, 14S/114P/291V/518Q/562S, 14S/114P/518Q, 14S/234L/283D/291V/305E, 14S/283D/289Q/562S, 29E/66N/111K/540R, 29E/111K, 29E/111K/523D, 29G/66N/111K, 33N/46R/49D/549D, 33N/46T/49D, 33N/46T/49D/336V/519E/548K/549D, 33N/46T/49D/549D, 33N/46T/518V/534S/548K/549D, 33N/46T/519E, 33N/49D/336V, 33N/336V/519P, 36V/37A/56G/59A/145V/234Y/328S, 36V/37A/59A/131M/531D, 36V/37A/103L/234Y, 36V/37A/131M/145V/234Y/328S, 36V/37A/145V/234Y, 36V/37A/145V/234Y/328S/471Y/531D, 36V/37A/234Y/328Q/531D, 36V/56G/145V/234Y/328S, 36V/59A/234Y/328S, 36V/59A/531D, 36V/103L/145V/328S/531D, 36V/131M, 36V/234Y/531D, 37A/56G/59A/103L/145V/234Y/328Q/471Y/531D, 37A/56G/59A/234Y/328S/524L/531D, 37A/56G/59A/234Y/531D, 37A/56G/234Y/531D, 37A/59A/234Y, 37A/234Y/471Y, 46R/49D, 46R/49D/518V/519E/548K/549D, 46R/49D/519P, 46R/155L, 46T/49D/519E, 46T/548K, 49D/519P, 56G/59A/103L/471Y/531D, 56G/59A/471Y/531D, 56R, 56R/114P/206P/283D, 56R/114P/291V, 56R/114P/291V/518Q/562S, 56R/114P/518Q, 56R/518Q, 59A/328Q/524L/531D, 66R/540R, 111K, 111K/510K/521D/523A/541A/558D, 111K/523A/557E, 114P, 114P/206P/283S/289Q/562S, 114P/283D/289Q/291V, 114P/283D/289Q/305E/518Q, 114P/283D/291V, 114P/289Q, 114P/289Q/562S, 114P/291V, 114P/291V/518Q, 114P/518Q/562S, 114P/562S, 131M/234Y/328Q, 234Y, 234Y/328Q, 234Y/328S/471Y, 234Y/531D, 289Q/562S, 305E, 336V/519P, 518V/519E/548K/549D, 519P, 521D, wherein the positions are numbered with reference to SEQ ID NO: 604. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from F14S/K56R/S114P, F14S/S114P/E283D/R289Q, F14S/S114P/E283D/R289Q/I291V, F14S/S114P/E283S/R289Q/I562S, F14S/S114P/I291V/K518Q/I562S, F14S/S114P/K518Q, F14S/H234L/E283D/I291V/Q305E, F14S/E283D/R289Q/I562S, P29E/Q66N/Q111K/A540R, P29E/Q111K, P29E/Q111K/E523D, P29G/Q66N/Q111K, K33N/L46R/T49D/G549D, K33N/L46T/T49D, K33N/L46T/T49D/I336V/A519E/S548K/G549D, K33N/L46T/T49D/G549D, K33N/L46T/K518V/A534S/S548K/G549D, K33N/L46T/A519E, K33N/T49D/I336V, K33N/I336V/A519P, A36V/Q37A/K56G/S59A/E145V/H234Y/A328S, A36V/Q37A/S59A/H131M/N531D, A36V/Q37A/R103L/H234Y, A36V/Q37A/H131M/E145V/H234Y/A328S, A36V/Q37A/E145V/H234Y, A36V/Q37A/E145V/H234Y/A328S/Q471Y/N531D, A36V/Q37A/H234Y/A328Q/N531D, A36V/K56G/E145V/H234Y/A328S, A36V/S59A/H234Y/A328S, A36V/S59A/N531D, A36V/R103L/E145V/A328S/N531D, A36V/H131M, A36V/H234Y/N531D, Q37A/K56G/S59A/R103L/E145V/H234Y/A328Q/Q471Y/N531D, Q37A/K56G/S59A/H234Y/A328S/R524L/N531D, Q37A/K56G/S59A/H234Y/N531D, Q37A/K56G/H234Y/N531D, Q37A/S59A/H234Y, Q37A/H234Y/Q471Y, L46R/T49D,

L46R/T49D/K518V/A519E/S548K/G549D, L46R/T49D/A519P, L46R/H155L, L46T/T49D/A519E, L46T/S548K, T49D/A519P, K56G/S59A/R103L/Q471Y/N531D, K56G/S59A/Q471Y/N531D, K56R, K56R/S114P/E206P/E283D, K56R/S114P/I291V, K56R/S114P/I291V/K518Q/I562S, K56R/S114P/K518Q, K56R/K518Q, S59A/A328Q/R524L/N531D, Q66R/A540R, Q111K, Q111K/L510K/S521D/E523A/L541A/Q558D, Q111K/E523A/N557E, S114P, S114P/E206P/E283S/R289Q/I562S, S114P/E283D/R289Q/I291V, S114P/E283D/R289Q/Q305E/K518Q, S114P/E283D/I291V, S114P/R289Q, S114P/R289Q/I562S, S114P/I291V, S114P/I291V/K518Q, S114P/K518Q/I562S, S114P/I562S, H131M/H234Y/A328Q, H234Y, H234Y/A328Q, H234Y/A328S/Q471Y, H234Y/N531D, R289Q/I562S, Q305E, I336V/A519P, K518V/A519E/S548K/G549D, A519P, S521D, E523D, N531D, L541A, S548K/G549D, and G549D, wherein the positions are numbered with reference to SEQ ID NO: 604.

[0020] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 20/49/56/59/111/291, 20/59/234/518/549/562, 49/56/59/66/291/531/549, 49/56/59/111/549, 49/56/66/111/234/291/518, 49/56/66/234, 49/59/66/145/234, 49/59/66/289, 49/59/289/562, 49/66/111/234/291/518/562, 49/111/531, 49/234, 56/59/111/234/289, 56/59/111/234/531, 56/59/111/283/518/531, 56/59/111/291, 56/59/111/291/518/531, 56/59/145/289/518/562, 56/59/234, 56/59/234/518, 56/59/518, 56/111/145/234/289/531/562, 56/111/145/234/518/549/562, 56/111/518/549, 56/234/291, 59, 59/111, 59/145/234/291, 59/234/291, 59/234/291/387/549/562, 111/145, 111/145/234/291/562, 111/145/234/562, 111/234, 111/289, 111/291, 111/518, 234, 234/518/549, 291/518/549, 518, 518/531/549/562, 531, and 549, wherein the positions are numbered with reference to SEQ ID NO: 736. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 20G/49D/56G/59A/111K/291V, 20G/59A/234Y/518Q/549D/562S, 49D/56G/59A/66N/291V/531D/549D, 49D/56G/59A/111K/549D, 49D/56G/66N/111K/234Y/291V/518Q, 49D/56G/66N/234Y, 49D/59A/66N/145V/234Y, 49D/59A/66N/289Q, 49D/59A/289Q/562S, 49D/66N/111K/234Y/291V/518Q/562S, 49D/111K/531D, 49D/234Y, 56G/59A/111K/234Y/289Q, 56G/59A/111K/234Y/531D, 56G/59A/111K/283D/518Q/531D, 56G/59A/111K/291V, 56G/59A/111K/291V/518Q/531D, 56G/59A/145V/289Q/518Q/562S, 56G/59A/234Y, 56G/59A/234Y/518Q, 56G/59A/518Q, 56G/111K/145V/234Y/289Q/531D/562S, 56G/111K/145V/234Y/518Q/549D/562S, 56G/111K/518Q/549D, 56G/234Y/291V, 59A, 59A/111K, 59A/145V/234Y/291V, 59A/234Y/291V, 59A/234Y/291V/387T/549D/562S, 111K/145V, 111K/145V/234Y/291V/562S, 111K/145V/234Y/562S, 111K/234Y, 111K/289Q, 111K/291V, 111K/518Q, 234Y, 234Y/518Q/549D, 291V/518Q/549D, 518Q, 518Q/531D/549D/562S, 531D, and 549D, wherein the positions are numbered with reference to SEQ ID NO: 736. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from D20G/T49D/R56G/S59A/Q111K/I291V, D20G/S59A/H234Y/K518Q/G549D/I562S,

T49D/R56G/S59A/Q66N/I291V/N531D/G549D, T49D/R56G/S59A/Q111K/G549D,
 T49D/R56G/Q66N/Q111K/H234Y/I291V/K518Q, T49D/R56G/Q66N/H234Y,
 T49D/S59A/Q66N/E145V/H234Y, T49D/S59A/Q66N/R289Q, T49D/S59A/R289Q/I562S,
 T49D/Q66N/Q111K/H234Y/I291V/K518Q/I562S, T49D/Q111K/N531D, T49D/H234Y,
 R56G/S59A/Q111K/H234Y/R289Q, R56G/S59A/Q111K/H234Y/N531D,
 R56G/S59A/Q111K/E283D/K518Q/N531D, R56G/S59A/Q111K/I291V,
 R56G/S59A/Q111K/I291V/K518Q/N531D, R56G/S59A/E145V/R289Q/K518Q/I562S,
 R56G/S59A/H234Y, R56G/S59A/H234Y/K518Q, R56G/S59A/K518Q,
 R56G/Q111K/E145V/H234Y/R289Q/N531D/I562S,
 R56G/Q111K/E145V/H234Y/K518Q/G549D/I562S, R56G/Q111K/K518Q/G549D,
 R56G/H234Y/I291V, S59A, S59A/Q111K, S59A/E145V/H234Y/I291V, S59A/H234Y/I291V,
 S59A/H234Y/I291V/I387T/G549D/I562S, Q111K/E145V, Q111K/E145V/H234Y/I291V/I562S,
 Q111K/E145V/H234Y/I562S, Q111K/H234Y, Q111K/R289Q, Q111K/I291V, Q111K/K518Q,
 H234Y, H234Y/K518Q/G549D, I291V/K518Q/G549D, K518Q, K518Q/N531D/G549D/I562S,
 N531D, and G549D, wherein the positions are numbered with reference to SEQ ID NO: 736.

[0021] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 33/37, 33/37/46/305, 33/37/103, 33/37/103/305, 33/37/103/305/336/541/548, 33/37/103/305/523/548, 33/37/103/305/548, 33/37/103/336/518/541/548, 33/37/103/471/519/548, 33/37/103/518/523/541, 33/37/103/519/523, 33/37/103/523, 33/37/103/540, 33/37/305, 33/37/305/328, 33/37/305/328/548, 33/37/305/336/471/541, 33/37/305/336/518/523, 33/37/305/336/521/523/548, 33/37/305/336/521/548, 33/37/305/336/541, 33/37/305/471/521/548, 33/37/305/523/540, 33/37/305/540, 33/37/305/541, 33/37/336, 33/37/336/540, 33/37/336/540/548, 33/37/471/523/540/548, 33/37/518/521/540, 33/37/518/521/548, 33/37/518/548, 33/37/521/548, 33/37/523, 33/37/523/540/548, 33/37/540, 33/37/548, 33/46, 33/46/66/305/521/523/540/548, 33/46/103/305/336/518/519/540, 33/46/103/305/336/548, 33/46/103/305/540, 33/46/103/540/548, 33/46/305, 33/46/305/336, 33/46/305/518/540/548, 33/46/336/471/519/523/548, 33/46/336/521, 33/46/336/521/523, 33/46/336/540, 33/46/336/540/548, 33/46/518/521/548, 33/46/521/548, 33/46/523, 33/46/541, 33/46/548, 33/103/336/518/521/548, 33/471/523/541, 37, 37/103, 37/103/305/336, 37/103/305/336/521/523/540/548, 37/103/305/336/523/540, 37/103/305/471, 37/103/305/471/540/548, 37/103/305/521/541/548, 37/103/305/540, 37/103/328/336/518/523/548, 37/103/328/521/541/548, 37/103/336, 37/103/336/521/541, 37/103/519/541/548, 37/103/540, 37/103/541/548, 37/305, 37/305/336, 37/305/336/521/540/548, 37/305/336/523/548, 37/305/336/540/548, 37/305/336/541/548, 37/305/471, 37/305/471/523/540/548, 37/305/471/540/548, 37/305/519/548, 37/305/521/523/540/548, 37/305/521/540, 37/305/521/541/548, 37/305/523/541/548, 37/305/541, 37/305/541/548, 37/305/548, 37/336, 37/336/471/541/548, 37/336/521/523, 37/336/521/523/548, 37/336/523/548, 37/336/540, 37/336/548, 37/471, 37/471/518,

37/471/518/519/523, 37/471/521/540/548, 37/519, 37/521/523/548, 37/521/540, 37/523/541, 37/523/548, 37/540, 37/540/548, 37/541, 37/548, 46, 46/49/59/111/523/531/549, 46/49/111/234/289/436/549, 46/49/111/234/289/531/549, 46/49/111/234/336, 46/49/111/234/336/523/549, 46/49/111/336/549, 46/49/234/289/336, 46/49/234/336/521/523/549, 46/49/234/540/549, 46/49/234/549, 46/49/289/523/531/549/562, 46/49/531/549, 46/59/234, 46/59/549/562, 46/103/305, 46/103/305/336/471/540/548, 46/103/305/336/523, 46/103/305/471/540/548, 46/103/305/520/540, 46/103/305/548, 46/103/523/548, 46/103/540/548, 46/103/541, 46/103/541/548, 46/103/548, 46/111/234/289/531/549, 46/111/234/521/549, 46/111/523/531/549, 46/234/289/549, 46/234/521/523/531/540/549, 46/234/549, 46/289/549, 46/305, 46/305/336, 46/305/336/518, 46/305/336/522, 46/305/336/548, 46/305/471, 46/305/523/548, 46/305/548, 46/336/521/523, 46/336/523/548, 46/336/540, 46/336/540/548, 46/521/523, 46/521/523/540, 46/521/523/549, 46/521/548, 46/523/540, 46/523/541/548, 46/541, 46/541/548, 46/548, 46/549, 49, 49/59/111/234/289/521, 49/59/111/289/523, 49/59/234/289/336, 49/59/234/289/336/523/531/549, 49/59/289/305/336, 49/59/289/336, 49/59/336, 49/59/521/531, 49/111, 49/111/234, 49/111/234/289/336/523/531/549, 49/111/234/289/521/523/531/549/562, 49/111/234/289/523/549, 49/111/234/336/521/523, 49/111/234/336/523/531, 49/111/234/523/531/549, 49/111/234/531, 49/111/234/549, 49/111/289, 49/111/289/336/521/549, 49/111/523/531/549, 49/111/531/549, 49/234, 49/234/289, 49/234/289/336/531/549, 49/234/289/523, 49/234/289/523/531/540, 49/234/289/523/549, 49/234/305/549, 49/234/521, 49/234/549, 49/289/305/336/523, 49/289/336, 49/289/336/521/531, 49/336/521/562, 49/521/531/549/562, 49/521/549, 49/523/549, 49/549, 59, 59/111/234/289/305/336/549, 59/111/234/289/305/549, 59/111/289, 59/111/336, 59/549, 103, 103/336/519/548, 103/521/523/540, 111/234/289, 111/234/289/523, 111/289/336/521, 111/289/336/523/549, 111/336/562, 111/521/523/549, 234, 234/289, 234/289/336/523, 234/289/523/531/549/562, 234/289/523/549, 234/289/531, 234/289/549, 234/336, 234/336/531/562, 234/521/523, 234/521/523/549, 234/523/531, 234/531/549, 234/540, 234/549, 234/562, 289, 289/336/549, 289/521/523, 289/521/523/540, 289/521/523/549, 289/523, 305/336/541/548, 336/548, 519/548, 521, 521/548, 521/549, 521/562, 523, 531/549, 540, and 549, wherein the positions are numbered with reference to SEQ ID NO: 736. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 33N/37A, 33N/37A/46R/305E, 33N/37A/103L, 33N/37A/103L/305E, 33N/37A/103L/305E/336V/541A/548K, 33N/37A/103L/305E/523D/548K, 33N/37A/103L/305E/548K, 33N/37A/103L/336V/518V/541A/548K, 33N/37A/103L/471Y/519P/548K, 33N/37A/103L/518V/523D/541A, 33N/37A/103L/519P/523D, 33N/37A/103L/523D, 33N/37A/103L/540R, 33N/37A/305E, 33N/37A/305E/328Q, 33N/37A/305E/328Q/548K, 33N/37A/305E/336V/471Y/541A, 33N/37A/305E/336V/518V/523D, 33N/37A/305E/336V/521D/523D/548K, 33N/37A/305E/336V/521D/548K, 33N/37A/305E/336V/541A, 33N/37A/305E/471Y/521D/548K, 33N/37A/305E/523D/540R,

33N/37A/305E/540R, 33N/37A/305E/541A, 33N/37A/336V, 33N/37A/336V/540R,
33N/37A/336V/540R/548K, 33N/37A/471Y/523D/540R/548K, 33N/37A/518V/521D/540R,
33N/37A/518V/521D/548K, 33N/37A/518V/548K, 33N/37A/521D/548K, 33N/37A/523D,
33N/37A/523D/540R/548K, 33N/37A/540R, 33N/37A/548K, 33N/46R,
33N/46R/66K/305E/521D/523D/540R/548K, 33N/46R/103L/305E/336V/518V/519P/540R,
33N/46R/103L/305E/336V/548K, 33N/46R/103L/305E/540R, 33N/46R/103L/540R/548K,
33N/46R/305E, 33N/46R/305E/336V, 33N/46R/305E/518V/540R/548K,
33N/46R/336V/471Y/519P/523D/548K, 33N/46R/336V/521D, 33N/46R/336V/521D/523D,
33N/46R/336V/540R, 33N/46R/336V/540R/548K, 33N/46R/518V/521D/548K,
33N/46R/521D/548K, 33N/46R/523D, 33N/46R/541A, 33N/46R/548K,
33N/103L/336V/518V/521D/548K, 33N/471Y/523D/541A, 37A, 37A/103L, 37A/103L/305E/336V,
37A/103L/305E/336V/521D/523D/540R/548K, 37A/103L/305E/336V/523D/540R,
37A/103L/305E/471Y, 37A/103L/305E/471Y/540R/548K, 37A/103L/305E/521D/541A/548K,
37A/103L/305E/540R, 37A/103L/328Q/336V/518V/523D/548K, 37A/103L/328Q/521D/541A/548K,
37A/103L/336V, 37A/103L/336V/521D/541A, 37A/103L/519P/541A/548K, 37A/103L/540R,
37A/103L/541A/548K, 37A/305E, 37A/305E/336V, 37A/305E/336V/521D/540R/548K,
37A/305E/336V/523D/548K, 37A/305E/336V/540R/548K, 37A/305E/336V/541A/548K,
37A/305E/471Y, 37A/305E/471Y/523D/540R/548K, 37A/305E/471Y/540R/548K,
37A/305E/519P/548K, 37A/305E/521D/523D/540R/548K, 37A/305E/521D/540R,
37A/305E/521D/541A/548K, 37A/305E/523D/541A/548K, 37A/305E/541A, 37A/305E/541A/548K,
37A/305E/548K, 37A/336V, 37A/336V/471Y/541A/548K, 37A/336V/521D/523D,
37A/336V/521D/523D/548K, 37A/336V/523D/548K, 37A/336V/540R, 37A/336V/548K, 37A/471Y,
37A/471Y/518V, 37A/471Y/518V/519P/523D, 37A/471Y/521D/540R/548K, 37A/519P,
37A/521D/523D/548K, 37A/521D/540R, 37A/523D/541A, 37A/523D/548K, 37A/540R,
37A/540R/548K, 37A/541A, 37A/548K, 46R, 46R/49D/59A/111K/523D/531D/549D,
46R/49D/111K/234Y/289Q/436V/549D, 46R/49D/111K/234Y/289Q/531D/549D,
46R/49D/111K/234Y/336V, 46R/49D/111K/234Y/336V/523D/549D, 46R/49D/111K/336V/549D,
46R/49D/234Y/289Q/336V, 46R/49D/234Y/336V/521D/523D/549D, 46R/49D/234Y/540R/549D,
46R/49D/234Y/549D, 46R/49D/289Q/523D/531D/549D/562S, 46R/49D/531D/549D,
46R/59A/234Y, 46R/59A/549D/562S, 46R/103L/305E, 46R/103L/305E/336V/471Y/540R/548K,
46R/103L/305E/336V/523D, 46R/103L/305E/471Y/540R/548K, 46R/103L/305E/520Q/540R,
46R/103L/305E/548K, 46R/103L/523D/548K, 46R/103L/540R/548K, 46R/103L/541A,
46R/103L/541A/548K, 46R/103L/548K, 46R/111K/234Y/289Q/531D/549D,
46R/111K/234Y/521D/549D, 46R/111K/523D/531D/549D, 46R/234Y/289Q/549S,
46R/234Y/521D/523D/531D/540R/549D, 46R/234Y/549D, 46R/289Q/549D, 46R/305E,
46R/305E/336V, 46R/305E/336V/518V, 46R/305E/336V/522E, 46R/305E/336V/548K,
46R/305E/471Y, 46R/305E/523D/548K, 46R/305E/548K, 46R/336V/521D/523D,

46R/336V/523D/548K, 46R/336V/540R, 46R/336V/540R/548K, 46R/521D/523D, 46R/521D/523D/540R, 46R/521D/523D/549D, 46R/521D/548K, 46R/523D/540R, 46R/523D/541A/548K, 46R/541A, 46R/541A/548K, 46R/548K, 46R/549D, 49D, 49D/59A/111K/234Y/289Q/521D, 49D/59A/111K/289Q/523D, 49D/59A/234Y/289Q/336V, 49D/59A/234Y/289Q/336V/523D/531D/549D, 49D/59A/289Q/305E/336V, 49D/59A/289Q/336V, 49D/59A/336V, 49D/59A/521D/531D, 49D/111K, 49D/111K/234Y, 49D/111K/234Y/289Q/336V/523D/531D/549D, 49D/111K/234Y/289Q/521D/523D/531D/549D/562S, 49D/111K/234Y/289Q/523D/549D, 49D/111K/234Y/336V/521D/523D, 49D/111K/234Y/336V/523D/531D, 49D/111K/234Y/523D/531D/549D, 49D/111K/234Y/531D, 49D/111K/234Y/549D, 49D/111K/289Q, 49D/111K/289Q/336V/521D/549D, 49D/111K/523D/531D/549D, 49D/111K/531D/549D, 49D/234Y, 49D/234Y/289Q, 49D/234Y/289Q/336V/531D/549D, 49D/234Y/289Q/523D, 49D/234Y/289Q/523D/531D/540R, 49D/234Y/289Q/523D/549D, 49D/234Y/305E/549D, 49D/234Y/521D, 49D/234Y/549D, 49D/289Q/305E/336V/523D, 49D/289Q/336V, 49D/289Q/336V/521D/531D, 49D/336V/521D/562S, 49D/521D/531D/549D/562S, 49D/521D/549D, 49D/523D/549D, 49D/549D, 59A, 59A/111K/234Y/289Q/305E/336V/549D, 59A/111K/234Y/289Q/305E/549D, 59A/111K/289Q, 59A/111K/336V, 59A/549D, 103L, 103L/336V/519P/548K, 103L/521D/523D/540R, 111K/234Y/289Q, 111K/234Y/289Q/523D, 111K/289Q/336V/521D, 111K/289Q/336V/523D/549D, 111K/336V/562S, 111K/521D/523D/549D, 234Y, 234Y/289Q, 234Y/289Q/336V/523D, 234Y/289Q/523D/531D/549D/562S, 234Y/289Q/523D/549D, 234Y/289Q/531D, 234Y/289Q/549D, 234Y/336V, 234Y/336V/531D/562S, 234Y/521D/523D, 234Y/521D/523D/549D, 234Y/523D/531D, 234Y/531D/549D, 234Y/540R, 234Y/549D, 234Y/562S, 289Q, 289Q/336V/549D, 289Q/521D/523D, 289Q/521D/523D/540R, 289Q/521D/523D/549D, 289Q/523D, 305E/336V/541A/548K, 336V/548K, 519P/548K, 521D, 521D/548K, 521D/549D, 521D/562S, 523D, 531D/549D, 540R, and 549D, wherein the positions are numbered with reference to SEQ ID NO: 736. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from K33N/Q37A, K33N/Q37A/L46R/Q305E, K33N/Q37A/R103L, K33N/Q37A/R103L/Q305E, K33N/Q37A/R103L/Q305E/I336V/L541A/S548K, K33N/Q37A/R103L/Q305E/E523D/S548K, K33N/Q37A/R103L/Q305E/S548K, K33N/Q37A/R103L/I336V/K518V/L541A/S548K, K33N/Q37A/R103L/Q471Y/A519P/S548K, K33N/Q37A/R103L/K518V/E523D/L541A, K33N/Q37A/R103L/A519P/E523D, K33N/Q37A/R103L/E523D, K33N/Q37A/R103L/A540R, K33N/Q37A/Q305E, K33N/Q37A/Q305E/A328Q, K33N/Q37A/Q305E/A328Q/S548K, K33N/Q37A/Q305E/I336V/Q471Y/L541A, K33N/Q37A/Q305E/I336V/K518V/E523D, K33N/Q37A/Q305E/I336V/S521D/E523D/S548K, K33N/Q37A/Q305E/I336V/S521D/S548K, K33N/Q37A/Q305E/I336V/L541A, K33N/Q37A/Q305E/Q471Y/S521D/S548K, K33N/Q37A/Q305E/E523D/A540R, K33N/Q37A/Q305E/A540R, K33N/Q37A/Q305E/L541A,

K33N/Q37A/I336V, K33N/Q37A/I336V/A540R, K33N/Q37A/I336V/A540R/S548K,
K33N/Q37A/Q471Y/E523D/A540R/S548K, K33N/Q37A/K518V/S521D/A540R,
K33N/Q37A/K518V/S521D/S548K, K33N/Q37A/K518V/S548K, K33N/Q37A/S521D/S548K,
K33N/Q37A/E523D, K33N/Q37A/E523D/A540R/S548K, K33N/Q37A/A540R,
K33N/Q37A/S548K, K33N/L46R, K33N/L46R/Q66K/Q305E/S521D/E523D/A540R/S548K,
K33N/L46R/R103L/Q305E/I336V/K518V/A519P/A540R,
K33N/L46R/R103L/Q305E/I336V/S548K, K33N/L46R/R103L/Q305E/A540R,
K33N/L46R/R103L/A540R/S548K, K33N/L46R/Q305E, K33N/L46R/Q305E/I336V,
K33N/L46R/Q305E/K518V/A540R/S548K, K33N/L46R/I336V/Q471Y/A519P/E523D/S548K,
K33N/L46R/I336V/S521D, K33N/L46R/I336V/S521D/E523D, K33N/L46R/I336V/A540R,
K33N/L46R/I336V/A540R/S548K, K33N/L46R/K518V/S521D/S548K, K33N/L46R/S521D/S548K,
K33N/L46R/E523D, K33N/L46R/L541A, K33N/L46R/S548K,
K33N/R103L/I336V/K518V/S521D/S548K, K33N/Q471Y/E523D/L541A, Q37A, Q37A/R103L,
Q37A/R103L/Q305E/I336V, Q37A/R103L/Q305E/I336V/S521D/E523D/A540R/S548K,
Q37A/R103L/Q305E/I336V/E523D/A540R, Q37A/R103L/Q305E/Q471Y,
Q37A/R103L/Q305E/Q471Y/A540R/S548K, Q37A/R103L/Q305E/S521D/L541A/S548K,
Q37A/R103L/Q305E/A540R, Q37A/R103L/A328Q/I336V/K518V/E523D/S548K,
Q37A/R103L/A328Q/S521D/L541A/S548K, Q37A/R103L/I336V,
Q37A/R103L/I336V/S521D/L541A, Q37A/R103L/A519P/L541A/S548K, Q37A/R103L/A540R,
Q37A/R103L/L541A/S548K, Q37A/Q305E, Q37A/Q305E/I336V,
Q37A/Q305E/I336V/S521D/A540R/S548K, Q37A/Q305E/I336V/E523D/S548K,
Q37A/Q305E/I336V/A540R/S548K, Q37A/Q305E/I336V/L541A/S548K, Q37A/Q305E/Q471Y,
Q37A/Q305E/Q471Y/E523D/A540R/S548K, Q37A/Q305E/Q471Y/A540R/S548K,
Q37A/Q305E/A519P/S548K, Q37A/Q305E/S521D/E523D/A540R/S548K,
Q37A/Q305E/S521D/A540R, Q37A/Q305E/S521D/L541A/S548K,
Q37A/Q305E/E523D/L541A/S548K, Q37A/Q305E/L541A, Q37A/Q305E/L541A/S548K,
Q37A/Q305E/S548K, Q37A/I336V, Q37A/I336V/Q471Y/L541A/S548K,
Q37A/I336V/S521D/E523D, Q37A/I336V/S521D/E523D/S548K, Q37A/I336V/E523D/S548K,
Q37A/I336V/A540R, Q37A/I336V/S548K, Q37A/Q471Y, Q37A/Q471Y/K518V,
Q37A/Q471Y/K518V/A519P/E523D, Q37A/Q471Y/S521D/A540R/S548K, Q37A/A519P,
Q37A/S521D/E523D/S548K, Q37A/S521D/A540R, Q37A/E523D/L541A, Q37A/E523D/S548K,
Q37A/A540R, Q37A/A540R/S548K, Q37A/L541A, Q37A/S548K, L46R,
L46R/T49D/S59A/Q111K/E523D/N531D/G549D,
L46R/T49D/Q111K/H234Y/R289Q/L436V/G549D,
L46R/T49D/Q111K/H234Y/R289Q/N531D/G549D, L46R/T49D/Q111K/H234Y/I336V,
L46R/T49D/Q111K/H234Y/I336V/E523D/G549D, L46R/T49D/Q111K/I336V/G549D,
L46R/T49D/H234Y/R289Q/I336V, L46R/T49D/H234Y/I336V/S521D/E523D/G549D,

L46R/T49D/H234Y/A540R/G549D, L46R/T49D/H234Y/G549D,
L46R/T49D/R289Q/E523D/N531D/G549D/I562S, L46R/T49D/N531D/G549D, L46R/S59A/H234Y,
L46R/S59A/G549D/I562S, L46R/R103L/Q305E,
L46R/R103L/Q305E/I336V/Q471Y/A540R/S548K, L46R/R103L/Q305E/I336V/E523D,
L46R/R103L/Q305E/Q471Y/A540R/S548K, L46R/R103L/Q305E/P520Q/A540R,
L46R/R103L/Q305E/S548K, L46R/R103L/E523D/S548K, L46R/R103L/A540R/S548K,
L46R/R103L/L541A, L46R/R103L/L541A/S548K, L46R/R103L/S548K,
L46R/Q111K/H234Y/R289Q/N531D/G549D, L46R/Q111K/H234Y/S521D/G549D,
L46R/Q111K/E523D/N531D/G549D, L46R/H234Y/R289Q/G549S,
L46R/H234Y/S521D/E523D/N531D/A540R/G549D, L46R/H234Y/G549D, L46R/R289Q/G549D,
L46R/Q305E, L46R/Q305E/I336V, L46R/Q305E/I336V/K518V, L46R/Q305E/I336V/K522E,
L46R/Q305E/I336V/S548K, L46R/Q305E/Q471Y, L46R/Q305E/E523D/S548K,
L46R/Q305E/S548K, L46R/I336V/S521D/E523D, L46R/I336V/E523D/S548K, L46R/I336V/A540R,
L46R/I336V/A540R/S548K, L46R/S521D/E523D, L46R/S521D/E523D/A540R,
L46R/S521D/E523D/G549D, L46R/S521D/S548K, L46R/E523D/A540R,
L46R/E523D/L541A/S548K, L46R/L541A, L46R/L541A/S548K, L46R/S548K, L46R/G549D,
T49D, T49D/S59A/Q111K/H234Y/R289Q/S521D, T49D/S59A/Q111K/R289Q/E523D,
T49D/S59A/H234Y/R289Q/I336V, T49D/S59A/H234Y/R289Q/I336V/E523D/N531D/G549D,
T49D/S59A/R289Q/Q305E/I336V, T49D/S59A/R289Q/I336V, T49D/S59A/I336V,
T49D/S59A/S521D/N531D, T49D/Q111K, T49D/Q111K/H234Y,
T49D/Q111K/H234Y/R289Q/I336V/E523D/N531D/G549D,
T49D/Q111K/H234Y/R289Q/S521D/E523D/N531D/G549D/I562S,
T49D/Q111K/H234Y/R289Q/E523D/G549D, T49D/Q111K/H234Y/I336V/S521D/E523D,
T49D/Q111K/H234Y/I336V/E523D/N531D, T49D/Q111K/H234Y/E523D/N531D/G549D,
T49D/Q111K/H234Y/N531D, T49D/Q111K/H234Y/G549D, T49D/Q111K/R289Q,
T49D/Q111K/R289Q/I336V/S521D/G549D, T49D/Q111K/E523D/N531D/G549D,
T49D/Q111K/N531D/G549D, T49D/H234Y, T49D/H234Y/R289Q,
T49D/H234Y/R289Q/I336V/N531D/G549D, T49D/H234Y/R289Q/E523D,
T49D/H234Y/R289Q/E523D/N531D/A540R, T49D/H234Y/R289Q/E523D/G549D,
T49D/H234Y/Q305E/G549D, T49D/H234Y/S521D, T49D/H234Y/G549D,
T49D/R289Q/Q305E/I336V/E523D, T49D/R289Q/I336V, T49D/R289Q/I336V/S521D/N531D,
T49D/I336V/S521D/I562S, T49D/S521D/N531D/G549D/I562S, T49D/S521D/G549D,
T49D/E523D/G549D, T49D/G549D, S59A, S59A/Q111K/H234Y/R289Q/Q305E/I336V/G549D,
S59A/Q111K/H234Y/R289Q/Q305E/G549D, S59A/Q111K/R289Q, S59A/Q111K/I336V,
S59A/G549D, R103L, R103L/I336V/A519P/S548K, R103L/S521D/E523D/A540R,
Q111K/H234Y/R289Q, Q111K/H234Y/R289Q/E523D, Q111K/R289Q/I336V/S521D,
Q111K/R289Q/I336V/E523D/G549D, Q111K/I336V/I562S, Q111K/S521D/E523D/G549D, H234Y,

H234Y/R289Q, H234Y/R289Q/I336V/E523D, H234Y/R289Q/E523D/N531D/G549D/I562S, H234Y/R289Q/E523D/G549D, H234Y/R289Q/N531D, H234Y/R289Q/G549D, H234Y/I336V, H234Y/I336V/N531D/I562S, H234Y/S521D/E523D, H234Y/S521D/E523D/G549D, H234Y/E523D/N531D, H234Y/N531D/G549D, H234Y/A540R, H234Y/G549D, H234Y/I562S, R289Q, R289Q/I336V/G549D, R289Q/S521D/E523D, R289Q/S521D/E523D/A540R, R289Q/S521D/E523D/G549D, R289Q/E523D, Q305E/I336V/L541A/S548K, I336V/S548K, A519P/S548K, S521D, S521D/S548K, S521D/G549D, S521D/I562S, E523D, N531D/G549D, A540R, and G549D, wherein the positions are numbered with reference to SEQ ID NO: 736.

[0022] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 24/44/464, 24/201/202/351/507, 24/202/351, 33/37/46/56/103/523/540/548/549, 33/37/46/56/111/234/523, 33/37/46/56/111/523/540, 33/37/46/103/111/234, 33/37/46/103/111/548/549, 33/37/46/103/523, 33/37/46/111/234/328/523/540/548, 33/37/46/111/336/540, 33/37/46/234/523, 33/37/46/336, 33/37/46/548/549, 33/37/56/111/234/523/540/548, 33/37/56/234/523/540/548, 33/37/103/111/234/336/540/548, 33/37/103/336/523/540/548, 33/37/111/234/523/540/548, 33/37/111/523/540, 33/37/111/548, 33/37/234/336/523/548, 33/37/523/540/548, 33/46, 33/46/56/111/548, 33/46/56/234/248/549, 33/46/103/523/549, 33/56/103/111, 33/103/111/234, 33/103/111/234/336/523/548, 33/103/111/234/540/549, 33/103/111/336, 33/111/234/548, 33/234/328/523/540/549, 33/234/336/523/540/548/549, 33/234/523/540/548, 33/234/523/548, 33/234/540/548/549, 33/336, 33/336/523/540/548/549, 33/336/540/548, 33/336/549, 37, 37/46/56/523, 37/46/234, 37/46/336/523/540/548, 37/46/336/540/548, 37/56/234/336/523/540/548/549, 37/56/336/523/540/548, 37/103/336/548/549, 37/111/523, 37/234/328/336/523, 37/336, 37/548/549, 44, 46/103/328/336/523, 46/103/336, 46/234/336, 46/234/540/548, 46/336/540/549, 202, 202/332/408, 234/523/540/548/549, 336/523, 408, and 523/548, wherein the positions are numbered with reference to SEQ ID NO: 790. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 24T/44R/464Q, 24T/201N/202R/351N/507R, 24T/202R/351N, 33N/37A/46R/56G/103L/523D/540R/548K/549D, 33N/37A/46R/56G/111K/234Y/523D, 33N/37A/46R/56G/111K/523D/540R, 33N/37A/46R/103L/111K/234Y, 33N/37A/46R/103L/111K/548K/549D, 33N/37A/46R/103L/523D, 33N/37A/46R/111K/234Y/328Q/523D/540R/548K, 33N/37A/46R/111K/336V/540R, 33N/37A/46R/234Y/523D, 33N/37A/46R/336V, 33N/37A/46R/548K/549D, 33N/37A/56G/111K/234Y/523D/540R/548K, 33N/37A/56G/234Y/523D/540R/548K, 33N/37A/103L/111K/234Y/336V/540R/548K, 33N/37A/103L/336V/523D/540R/548K, 33N/37A/111K/234Y/523D/540R/548K, 33N/37A/111K/523D/540R, 33N/37A/111K/548K, 33N/37A/234Y/336V/523D/548K, 33N/37A/523D/540R/548K, 33N/46R, 33N/46R/56G/111K/548K, 33N/46R/56G/234Y/248V/549D, 33N/46R/103L/523D/549D, 33N/56G/103L/111K,

33N/103L/111K/234Y, 33N/103L/111K/234Y/336V/523D/548K, 33N/103L/111K/234Y/540R/549D, 33N/103L/111K/336V, 33N/111K/234Y/548K, 33N/234Y/328Q/523D/540R/549D, 33N/234Y/336V/523D/540R/548K/549D, 33N/234Y/523D/540R/548K, 33N/234Y/523D/548K, 33N/234Y/540R/548K/549D, 33N/336V, 33N/336V/523D/540R/548K/549D, 33N/336V/540R/548K, 33N/336V/549D, 37A, 37A/46R/56G/523D, 37A/46R/234Y, 37A/46R/336V/523D/540R/548K, 37A/46R/336V/540R/548K, 37A/56G/234Y/336V/523D/540R/548K/549D, 37A/56G/336V/523D/540R/548K, 37A/103L/336V/548K/549D, 37A/111K/523D, 37A/234Y/328Q/336V/523D, 37A/336V, 37A/548K/549D, 44R, 46R/103L/328Q/336V/523D, 46R/103L/336V, 46R/234Y/336V, 46R/234Y/540R/548K, 46R/336V/540R/549D, 202R, 202R/332Q/408E, 234Y/523D/540R/548K/549D, 336V/523D, 408E, and 523D/548K, wherein the positions are numbered with reference to SEQ ID NO: 790. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from I24T/K44R/R464Q, I24T/K201N/L202R/G351N/Q507R, I24T/L202R/G351N, K33N/Q37A/L46R/R56G/R103L/E523D/A540R/S548K/G549D, K33N/Q37A/L46R/R56G/Q111K/H234Y/E523D, K33N/Q37A/L46R/R56G/Q111K/E523D/A540R, K33N/Q37A/L46R/R103L/Q111K/H234Y, K33N/Q37A/L46R/R103L/Q111K/S548K/G549D, K33N/Q37A/L46R/R103L/E523D, K33N/Q37A/L46R/Q111K/H234Y/A328Q/E523D/A540R/S548K, K33N/Q37A/L46R/Q111K/I336V/A540R, K33N/Q37A/L46R/H234Y/E523D, K33N/Q37A/L46R/I336V, K33N/Q37A/L46R/S548K/G549D, K33N/Q37A/R56G/Q111K/H234Y/E523D/A540R/S548K, K33N/Q37A/R56G/H234Y/E523D/A540R/S548K, K33N/Q37A/R103L/Q111K/H234Y/I336V/A540R/S548K, K33N/Q37A/R103L/I336V/E523D/A540R/S548K, K33N/Q37A/Q111K/H234Y/E523D/A540R/S548K, K33N/Q37A/Q111K/E523D/A540R, K33N/Q37A/Q111K/S548K, K33N/Q37A/H234Y/I336V/E523D/S548K, K33N/Q37A/E523D/A540R/S548K, K33N/L46R, K33N/L46R/R56G/Q111K/S548K, K33N/L46R/R56G/H234Y/A248V/G549D, K33N/L46R/R103L/E523D/G549D, K33N/R56G/R103L/Q111K, K33N/R103L/Q111K/H234Y, K33N/R103L/Q111K/H234Y/I336V/E523D/S548K, K33N/R103L/Q111K/H234Y/A540R/G549D, K33N/R103L/Q111K/I336V, K33N/Q111K/H234Y/S548K, K33N/H234Y/A328Q/E523D/A540R/G549D, K33N/H234Y/I336V/E523D/A540R/S548K/G549D, K33N/H234Y/E523D/A540R/S548K, K33N/H234Y/E523D/S548K, K33N/H234Y/A540R/S548K/G549D, K33N/I336V, K33N/I336V/E523D/A540R/S548K/G549D, K33N/I336V/A540R/S548K, K33N/I336V/G549D, Q37A, Q37A/L46R/R56G/E523D, Q37A/L46R/H234Y, Q37A/L46R/I336V/E523D/A540R/S548K, Q37A/L46R/I336V/A540R/S548K, Q37A/R56G/H234Y/I336V/E523D/A540R/S548K/G549D,

Q37A/R56G/I336V/E523D/A540R/S548K, Q37A/R103L/I336V/S548K/G549D, Q37A/Q111K/E523D, Q37A/H234Y/A328Q/I336V/E523D, Q37A/I336V, Q37A/S548K/G549D, K44R, L46R/R103L/A328Q/I336V/E523D, L46R/R103L/I336V, L46R/H234Y/I336V, L46R/H234Y/A540R/S548K, L46R/I336V/A540R/G549D, L202R, L202R/K332Q/D408E, H234Y/E523D/A540R/S548K/G549D, I336V/E523D, D408E, and E523D/S548K, wherein the positions are numbered with reference to SEQ ID NO: 790.

[0023] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 74, 102, 210, 313, 391, 392, 402, 415, 417, 418, 420, 424, 506, and 530, wherein the positions are numbered with reference to SEQ ID NO: 790. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 74A, 102P, 210T, 313I, 313M, 391N, 392A, 402A, 415F, 417A, 418V, 420L, 424A, 506C, and 530V, wherein the positions are numbered with reference to SEQ ID NO: 790. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from I74A, M102P, L210T, L313I, L313M, T391N, M392A, S402A, L415F, G417A, L418V, I420L, S424A, R506C, and D530V, wherein the positions are numbered with reference to SEQ ID NO: 790.

[0024] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 24, 24/44, 24/44/46/202/391, 24/44/111/202/464/506, 24/44/202/313/391/540, 24/44/549, 24/46/102/313/506, 24/46/103/111/464/506/549, 24/46/103/391/506, 24/46/111/313/391, 24/46/111/313/549, 24/46/111/506, 24/46/202/391/506, 24/46/549, 24/103/202, 24/202, 44/46/102/202/313/417, 44/46/103/111/391, 44/46/103/202/313/391, 44/46/103/202/417/464, 44/103/111/313/391/540, 44/111/464/506, 46/103/506, 46/111/417, 46/111/506, 46/202, 46/202/506/549, 46/313/391/540, 103/313/549, 111, 111/202, 111/202/313/391/464, 111/202/313/391/506, 111/202/313/417/540/549, 111/202/391, 111/202/391/540, 111/464/540/549, 202/313/391/549, 202/417/464/540/549, 202/464/506, 202/506/540, 202/506/540/549, 313/391/540/549, and 417, wherein the positions are numbered with reference to SEQ ID NO: 1454. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 24T, 24T/44R, 24T/44R/46R/202R/391N, 24T/44R/111K/202R/464Q/506C, 24T/44R/202R/313M/391N/540R, 24T/44R/549D, 24T/46R/102P/313M/506C, 24T/46R/103L/111K/464Q/506C/549D, 24T/46R/103L/391N/506C, 24T/46R/111K/313M/391N, 24T/46R/111K/313M/549D, 24T/46R/111K/506C, 24T/46R/202R/391N/506C, 24T/46R/549D, 24T/103L/202R, 24T/202R, 44R/46R/102P/202R/313M/417A, 44R/46R/103L/111K/391N, 44R/46R/103L/202R/313M/391N, 44R/46R/103L/202R/417A/464Q, 44R/103L/111K/313M/391N/540R, 44R/111K/464Q/506C, 46R/103L/506C, 46R/111K/417A, 46R/111K/506C, 46R/202R, 46R/202R/506C/549D, 46R/313M/391N/540R, 103L/313M/549D, 111K, 111K/202R, 111K/202R/313M/391N/464Q, 111K/202R/313M/391N/506C, 111K/202R/313M/417A/540R/549D, 111K/202R/391N,

111K/202R/391N/540R, 111K/464Q/540R/549D, 202R/313M/391N/549D, 202R/417A/464Q/540R/549D, 202R/464Q/506C, 202R/506C/540R, 202R/506C/540R/549D, 313M/391N/540R/549D, and 417A, wherein the positions are numbered with reference to SEQ ID NO: 1454. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from I24T, I24T/K44R, I24T/K44R/L46R/L202R/T391N, I24T/K44R/Q111K/L202R/R464Q/R506C, I24T/K44R/L202R/L313M/T391N/A540R, I24T/K44R/G549D, I24T/L46R/M102P/L313M/R506C, I24T/L46R/R103L/Q111K/R464Q/R506C/G549D, I24T/L46R/R103L/T391N/R506C, I24T/L46R/Q111K/L313M/T391N, I24T/L46R/Q111K/L313M/G549D, I24T/L46R/Q111K/R506C, I24T/L46R/L202R/T391N/R506C, I24T/L46R/G549D, I24T/R103L/L202R, I24T/L202R, K44R/L46R/M102P/L202R/L313M/G417A, K44R/L46R/R103L/Q111K/T391N, K44R/L46R/R103L/L202R/L313M/T391N, K44R/L46R/R103L/L202R/G417A/R464Q, K44R/R103L/Q111K/L313M/T391N/A540R, K44R/Q111K/R464Q/R506C, L46R/R103L/R506C, L46R/Q111K/G417A, L46R/Q111K/R506C, L46R/L202R, L46R/L202R/R506C/G549D, L46R/L313M/T391N/A540R, R103L/L313M/G549D, Q111K, Q111K/L202R, Q111K/L202R/L313M/T391N/R464Q, Q111K/L202R/L313M/T391N/R506C, Q111K/L202R/L313M/G417A/A540R/G549D, Q111K/L202R/T391N, Q111K/L202R/T391N/A540R, Q111K/R464Q/A540R/G549D, L202R/L313M/T391N/G549D, L202R/G417A/R464Q/A540R/G549D, L202R/R464Q/R506C, L202R/R506C/A540R, L202R/R506C/A540R/G549D, L313M/T391N/A540R/G549D, and G417A, wherein the positions are numbered with reference to SEQ ID NO: 1454.

[0025] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 20/44/202/506, 20/103/111/471/506, 20/202/313/471/506, 24, 27, 33, 36, 41, 44, 44/111/202/464/471/506/549, 44/202/464/506, 46, 48, 50, 51, 55, 56/111/506, 56/506, 59, 66, 66/528, 103/111/202/464/471, 103/111/471, 103/202/540, 103/464/549, 103/471, 111, 111/202/313/316, 111/202/313/471/506, 111/202/471, 111/506, 197, 202, 202/313/464/471/506, 202/464/506, 202/464/506/549, 208, 272, 289, 292/553, 305, 312/559, 313/464/471/506, 331, 332, 432, 435, 464, 464/506, 470, 500, 504, 506, 506/549, 518, 519, 523, 540, 543, 547, 547/553, 555, 556, and 559, wherein the positions are numbered with reference to SEQ ID NO: 1578. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 20G/44R/202R/506R, 20G/103L/111K/471Y/506R, 20G/202R/313L/471Y/506R, 24E, 24K, 24Q, 24S, 27S, 33E, 36S, 36T, 41A, 41H, 41L, 41N, 41Q, 41S, 44E, 44P, 44R, 44R/111K/202R/464Q/471Y/506R/549D, 44R/202R/464Q/506R, 44S, 46A, 46S, 48A, 48G, 50M, 51A, 51H, 55S, 56G/111K/506R, 56G/506R, 59N, 59S, 66H/528R, 66K, 66N, 66T, 103L/111K/202R/464Q/471Y, 103L/111K/471Y, 103L/202R/540R, 103L/464Q/549D, 103L/471Y, 111K, 111K/202R/313L/316Q, 111K/202R/313L/471Y/506R, 111K/202R/471Y, 111K/506R, 197V, 202R,

202R/313L/464Q/471Y/506R, 202R/464Q/506R, 202R/464Q/506R/549D, 208M, 272A, 289L, 292L/553S, 305D, 305E, 312C/559Y, 313L/464Q/471Y/506R, 331G, 332N, 432L, 432T, 435A, 435T, 464N, 464Q/506R, 464S, 470I, 470T, 500L, 504A, 504L, 506E, 506R, 506R/549D, 518S, 519E, 519K, 519P, 519T, 523H, 540H, 540R, 543T, 543V, 547G, 547M/553I, 555S, 556L, 556V, 559C, 559H, 559I, 559L, 559M, and 559Y, wherein the positions are numbered with reference to SEQ ID NO: 1578. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from D20G/K44R/L202R/C506R, D20G/R103L/Q111K/Q471Y/C506R, D20G/L202R/M313L/Q471Y/C506R, T24E, T24K, T24Q, T24S, D27S, N33E, A36S, A36T, Y41A, Y41H, Y41L, Y41N, Y41Q, Y41S, K44E, K44P, K44R, K44R/Q111K/L202R/R464Q/Q471Y/C506R/G549D, K44R/L202R/R464Q/C506R, K44S, R46A, R46S, T48A, T48G, K50M, E51A, E51H, Q55S, R56G/Q111K/C506R, R56G/C506R, A59N, A59S, Q66H/W528R, Q66K, Q66N, Q66T, R103L/Q111K/L202R/R464Q/Q471Y, R103L/Q111K/Q471Y, R103L/L202R/A540R, R103L/R464Q/G549D, R103L/Q471Y, Q111K, Q111K/L202R/M313L/L316Q, Q111K/L202R/M313L/Q471Y/C506R, Q111K/L202R/Q471Y, Q111K/C506R, P197V, L202R, L202R/M313L/R464Q/Q471Y/C506R, L202R/R464Q/C506R, L202R/R464Q/C506R/G549D, L208M, P272A, Q289L, R292L/V553S, Q305D, Q305E, S312C/V559Y, M313L/R464Q/Q471Y/C506R, A331G, K332N, Y432L, Y432T, S435A, S435T, R464N, R464Q/C506R, R464S, Q470I, Q470T, C500L, R504A, R504L, C506E, C506R, C506R/G549D, K518S, A519E, A519K, A519P, A519T, D523H, A540H, A540R, A543T, A543V, T547G, T547M/V553I, A555S, I556L, I556V, V559C, V559H, V559I, V559L, V559M, and V559Y, wherein the positions are numbered with reference to SEQ ID NO: 1578.

[0026] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 20, 20/44/208/272/519, 20/111/208/272/410/432, 20/197/432/519, 24, 24/46/410/435/518, 36/55/305/332/410, 36/66/197/305/332/457, 36/66/197/305/410, 36/66/305, 36/66/305/332/410, 36/66/305/500, 36/197/305, 36/197/305/332/410, 36/197/305/332/410/500, 36/197/305/332/410/559, 36/197/305/332/500, 36/197/305/410, 36/197/305/500, 36/305, 36/305/332, 36/305/332/410, 36/305/410, 41/44/46/111/272, 41/432/526, 44/46/111/208, 44/46/111/432/519, 44/111/432/519/526, 44/208/432/435, 46/111/208/272/435/526, 46/208/272/432/435/526, 46/432/471, 55/305, 55/305/332/457/543/547, 55/305/500/559, 66/305, 66/305/332, 111, 111/272/432/435, 111/272/471/526, 111/272/519, 111/432/435, 111/432/526, 111/526, 134/202/305, 197/305, 197/305/332/410, 197/305/332/500/543/547, 197/305/410, 197/305/500, 208, 208/272/432, 208/410/435, 208/435/519, 211/410, 272, 272/435/526, 298/410, 305, 305/332, 305/332/410, 305/332/410/500, 305/332/457, 305/332/457/500, 305/332/457/555, 305/332/500, 305/410, 305/500/543/547, 410, 432/526, 435, 435/518, 435/519/526, 471, 471/526, and 519, wherein the positions are numbered with reference to SEQ ID NO: 1660. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 20G,

20G/44E/208M/272A/519K, 20G/111K/208M/272A/410M/432T, 20G/197V/432T/519K, 24E, 24E/46S/410M/435T/518S, 36S/55S/305D/332N/410M, 36S/66N/197V/305D/332N/457S, 36S/66N/197V/305D/410M, 36S/66N/305D, 36S/66N/305D/332N/410M, 36S/66N/305D/500L, 36S/197V/305D, 36S/197V/305D/332N/410M, 36S/197V/305D/332N/410M/500L, 36S/197V/305D/332N/410M/559I, 36S/197V/305D/332N/500L, 36S/197V/305D/410M, 36S/197V/305D/500L, 36S/305D, 36S/305D/332N, 36S/305D/332N/410M, 36S/305D/410M, 41L/44E/46S/111K/272A, 41L/432T/526L, 44E/46S/111K/208M, 44E/46S/111K/432T/519K, 44E/111K/432L/519K/526L, 44E/208M/432T/435T, 46S/111K/208M/272A/435T/526L, 46S/208M/272A/432L/435T/526L, 46S/432L/471Y, 55S/305D, 55S/305D/332N/457S/543V/547G, 55S/305D/500L/559I, 66N/305D, 66N/305D/332N, 111K, 111K/272A/432T/435T, 111K/272A/471Y/526L, 111K/272A/519K, 111K/432L/435T, 111K/432T/526L, 111K/526L, 134C/202L/305D, 197V/305D, 197V/305D/332N/410M, 197V/305D/332N/500L/543V/547G, 197V/305D/410M, 197V/305D/500L, 208M, 208M/272A/432L, 208M/410M/435T, 208M/435T/519K, 211Q/410I, 272A, 272A/435T/526L, 298G/410I, 305D, 305D/332N, 305D/332N/410M, 305D/332N/410M/500L, 305D/332N/457S, 305D/332N/457S/500L, 305D/332N/457S/555S, 305D/332N/500L, 305D/410M, 305D/500L/543V/547G, 410L, 432L/526L, 435T, 435T/518S, 435T/519K/526L, 471Y, 471Y/526L, and 519K, wherein the positions are numbered with reference to SEQ ID NO: 1660. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from D20G, D20G/K44E/L208M/P272A/A519K, D20G/Q111K/L208M/P272A/P410M/Y432T, D20G/P197V/Y432T/A519K, T24E, T24E/R46S/P410M/S435T/K518S, A36S/Q55S/Q305D/K332N/P410M, A36S/Q66N/P197V/Q305D/K332N/G457S, A36S/Q66N/P197V/Q305D/P410M, A36S/Q66N/Q305D, A36S/Q66N/Q305D/K332N/P410M, A36S/Q66N/Q305D/C500L, A36S/P197V/Q305D, A36S/P197V/Q305D/K332N/P410M, A36S/P197V/Q305D/K332N/P410M/C500L, A36S/P197V/Q305D/K332N/P410M/V559I, A36S/P197V/Q305D/K332N/C500L, A36S/P197V/Q305D/P410M, A36S/P197V/Q305D/C500L, A36S/Q305D, A36S/Q305D/K332N, A36S/Q305D/K332N/P410M, A36S/Q305D/P410M, Y41L/K44E/R46S/Q111K/P272A, Y41L/Y432T/Y526L, K44E/R46S/Q111K/L208M, K44E/R46S/Q111K/Y432T/A519K, K44E/Q111K/Y432L/A519K/Y526L, K44E/L208M/Y432T/S435T, R46S/Q111K/L208M/P272A/S435T/Y526L, R46S/L208M/P272A/Y432L/S435T/Y526L, R46S/Y432L/Q471Y, Q55S/Q305D, Q55S/Q305D/K332N/G457S/A543V/T547G, Q55S/Q305D/C500L/V559I, Q66N/Q305D, Q66N/Q305D/K332N, Q111K, Q111K/P272A/Y432T/S435T, Q111K/P272A/Q471Y/Y526L, Q111K/P272A/A519K, Q111K/Y432L/S435T, Q111K/Y432T/Y526L, Q111K/Y526L, S134C/R202L/Q305D, P197V/Q305D, P197V/Q305D/K332N/P410M, P197V/Q305D/K332N/C500L/A543V/T547G, P197V/Q305D/P410M, P197V/Q305D/C500L, L208M, L208M/P272A/Y432L, L208M/P410M/S435T, L208M/S435T/A519K, L211Q/P410I,

P272A, P272A/S435T/Y526L, S298G/P410L, Q305D, Q305D/K332N, Q305D/K332N/P410M, Q305D/K332N/P410M/C500L, Q305D/K332N/G457S, Q305D/K332N/G457S/C500L, Q305D/K332N/G457S/A555S, Q305D/K332N/C500L, Q305D/P410M, Q305D/C500L/A543V/T547G, P410L, Y432L/Y526L, S435T, S435T/K518S, S435T/A519K/Y526L, Q471Y, Q471Y/Y526L, and A519K, wherein the positions are numbered with reference to SEQ ID NO: 1660.

[0027] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 24/59/111/289/504, 24/111/289, 24/111/289/500/504, 24/111/432, 24/111/435/500, 24/289, 24/432/435/504, 41/44/208/547, 41/51/410/543, 41/208/410/543/547, 41/208/518/519/547, 41/208/547, 41/410/518/543, 41/410/518/547, 41/543, 44/208/518/547, 51/519, 59/66/111/289/432/500, 59/66/111/432/500, 59/66/111/432/504, 59/66/289/500/504/556, 59/111, 59/111/432/500, 59/289, 59/289/435, 59/432, 59/432/435/504/556, 66/111, 111, 111/289, 111/289/435, 111/289/435/500, 111/289/500, 111/331/432/504, 111/331/435/500, 111/432, 111/432/500, 111/500/504, 208, 208/211/410/519, 208/211/547, 211, 211/518/519/547, 211/547, 289, 289/432, 289/432/435, 289/435, 289/435/500/504, 289/435/504/556, 289/504, 410, 432, 435/504, 504, 504/556, 519, and 547, wherein the positions are numbered with reference to SEQ ID NO: 1844.

[0028] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 24K/59S/111K/289L/504A, 24K/111K/289L, 24K/111K/289L/500L/504A, 24K/111K/432L, 24K/111K/435T/500L, 24K/289L, 24K/432L/435T/504A, 41Q/44P/208M/547G, 41Q/51A/410L/543V, 41Q/208M/410L/543V/547G, 41Q/208M/518S/519T/547G, 41Q/208M/547G, 41Q/410L/518S/543V, 41Q/410L/518S/547G, 41Q/543V, 44R/208M/518S/547G, 51A/519T, 59S/66T/111K/289L/432L/500L, 59S/66T/111K/432L/500L, 59S/66T/111K/432L/504A, 59S/66T/289L/500L/504A/556L, 59S/111K, 59S/111K/432L/500L, 59S/289L, 59S/289L/435T, 59S/432L, 59S/432L/435T/504A/556L, 66T/111K, 111K, 111K/289L, 111K/289L/435T, 111K/289L/435T/500L, 111K/289L/500L, 111K/331G/432L/504A, 111K/331G/435T/500L, 111K/432L, 111K/432L/500L, 111K/500L/504A, 208M, 208M/211Q/410L/519T, 208M/211Q/547G, 211Q, 211Q/518S/519T/547G, 211Q/547G, 289L, 289L/432L, 289L/432L/435T, 289L/435T, 289L/435T/500L/504A, 289L/435T/504A/556L, 289L/504A, 410L, 432L, 435T/504A, 504A, 504A/556L, 519T, and 547G, wherein the positions are numbered with reference to SEQ ID NO: 1844. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from

T24K/A59S/Q111K/Q289L/R504A, T24K/Q111K/Q289L, T24K/Q111K/Q289L/C500L/R504A, T24K/Q111K/Y432L, T24K/Q111K/S435T/C500L, T24K/Q289L, T24K/Y432L/S435T/R504A, Y41Q/K44P/L208M/T547G, Y41Q/E51A/M410L/A543V, Y41Q/L208M/M410L/A543V/T547G, Y41Q/L208M/K518S/A519T/T547G, Y41Q/L208M/T547G, Y41Q/M410L/K518S/A543V, Y41Q/M410L/K518S/T547G, Y41Q/A543V, K44R/L208M/K518S/T547G, E51A/A519T,

A59S/Q66T/Q111K/Q289L/Y432L/C500L, A59S/Q66T/Q111K/Y432L/C500L, A59S/Q66T/Q111K/Y432L/R504A, A59S/Q66T/Q289L/C500L/R504A/I556L, A59S/Q111K, A59S/Q111K/Y432L/C500L, A59S/Q289L, A59S/Q289L/S435T, A59S/Y432L, A59S/Y432L/S435T/R504A/I556L, Q66T/Q111K, Q111K, Q111K/Q289L, Q111K/Q289L/S435T, Q111K/Q289L/S435T/C500L, Q111K/Q289L/C500L, Q111K/A331G/Y432L/R504A, Q111K/A331G/S435T/C500L, Q111K/Y432L, Q111K/Y432L/C500L, Q111K/C500L/R504A, L208M, L208M/L211Q/M410L/A519T, L208M/L211Q/T547G, L211Q, L211Q/K518S/A519T/T547G, L211Q/T547G, Q289L, Q289L/Y432L, Q289L/Y432L/S435T, Q289L/S435T, Q289L/S435T/C500L/R504A, Q289L/S435T/R504A/I556L, Q289L/R504A, M410L, Y432L, S435T/R504A, R504A, R504A/I556L, A519T, and T547G, wherein the positions are numbered with reference to SEQ ID NO: 1844.

[0029] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 4, 8, 11, 13, 13/22/45/512, 13/45, 13/45/512, 17, 19, 45, 45/244/324/513, 45/436/512/513, 45/512, 144, 251, 324, 327, 341, and 428, wherein the positions are numbered with reference to SEQ ID NO: 2030. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 4D, 8D, 8G, 8R, 11A, 11D, 11G, 11K, 11S, 13Q/45V/512V, 13R, 13S/22T/45V/512V, 13S/45V, 17Q, 19H, 45V, 45V/244M/324V/513R, 45V/436I/512V/513R, 45V/512V, 144L, 251V, 324R, 327M, 341A, and 428V, wherein the positions are numbered with reference to SEQ ID NO: 2030. In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from A4D, Q8D, Q8G, Q8R, T11A, T11D, T11G, T11K, T11S, K13Q/A45V/I512V, K13R, K13S/V22T/A45V/I512V, K13S/A45V, T17Q, S19H, A45V, A45V/L244M/A324V/K513R, A45V/L436I/I512V/K513R, A45V/I512V, I144L, L251V, A324R, I327M, V341A, and L428V, wherein the positions are numbered with reference to SEQ ID NO: 2030.

[0030] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 2, 4, 4/8/11/13/22/111/504, 4/8/11/17/324/428/504, 4/8/11/22/111, 4/8/22/111/504, 4/17/241/519/547, 4/324, 4/428, 6, 7, 8/11/13/324, 8/11/17/22/324/504/519, 8/11/111/504, 10, 11/13/504, 11/17/22/324, 14, 16, 39, 57, 228, 228/259, 236, 305/307/425, 316, 385, 425, 430, 437, 478, and 505, wherein the positions are numbered with reference to SEQ ID NO: 2114.

[0031] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 2G, 2T, 4D, 4D/8D/11G/17P/324V/428V/504A, 4D/8D/22T/111K/504A, 4D/8R/11D/13R/22T/111K/504A, 4D/8R/11D/22T/111K, 4D/17Q/241S/519T/547A, 4D/324V, 4D/428V, 6G, 7Q, 8D/11D/13R/324V, 8D/11D/17Q/22T/324V/504A/519T, 8D/11D/111K/504A, 10G, 11D/17Q/22T/324V, 11G/13R/504A, 14G, 16Q, 16T, 39S, 57I, 228M, 228M/259H, 236V, 305E/307N/425V, 316T, 385A, 425V, 430E, 437G, 478L, and 505S, wherein the positions are numbered with reference to SEQ ID NO: 2114. In

some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from I2G, I2T, A4D, A4D/Q8D/T11G/T17P/A324V/L428V/R504A, A4D/Q8D/V22T/Q111K/R504A, A4D/Q8R/T11D/K13R/V22T/Q111K/R504A, A4D/Q8R/T11D/V22T/Q111K, A4D/T17Q/A241S/A519T/T547A, A4D/A324V, A4D/L428V, Q6G, T7Q, Q8D/T11D/K13R/A324V, Q8D/T11D/T17Q/V22T/A324V/R504A/A519T, Q8D/T11D/Q111K/R504A, F10G, T11D/T17Q/V22T/A324V, T11G/K13R/R504A, S14G, H16Q, H16T, A39S, V57I, I228M, I228M/Q259H, A236V, D305E/I307N/I425V, L316T, V385A, I425V, T430E, T437G, M478L, and T505S, wherein the positions are numbered with reference to SEQ ID NO: 2114.

[0032] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution set at one or more amino acid positions selected from 4/7/57/111, 4/7/111/114/437/547, 4/16/385/478, 4/57/111/437, 7/385/547, 10/16/437, 16, 16/41/57/111/385/547, 16/41/57/437/478, 16/41/437, 16/57, 16/241/437, 16/385, 16/385/437, 16/385/478/547, 16/437, 20/385/437/478/547, 57, 57/111/114, 57/111/478/547, 57/437, 111/114/202/234/289/305/313/324/332/336/410/432/435/464/504/512/519/523/548/549, 111/241/437/478, 111/478, 241, 241/385, 241/385/478, 241/385/478/547, 241/437, 385, 385/437, 385/437/478/547, 437, 437/478, and 478, wherein the positions are numbered with reference to SEQ ID NO: 2156.

[0033] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from 4D/7Q/57I/111K, 4D/7Q/111K/114S/437G/547G, 4D/16Q/385A/478L, 4D/57I/111K/437G, 7Q/385A/547G, 10G/16Q/437G, 16Q, 16Q/41Q/57I/111K/385A/547G, 16Q/41Q/57I/437G/478L, 16Q/41Q/437G, 16Q/57I, 16Q/241S/437G, 16Q/385A, 16Q/385A/437G, 16Q/385A/478L/547G, 16Q/437G, 20G/385A/437G/478L/547G, 57I, 57I/111K/114S, 57I/111K/478L/547G, 57I/437G, 111K/114S/202L/234H/289Q/305Q/313L/324A/332K/336I/410P/432Y/435S/464R/504R/512I/519A/523E/548S/549G, 111K/241S/437G/478L, 111K/478L, 241S, 241S/385A, 241S/385A/478L, 241S/385A/478L/547G, 241S/437G, 385A, 385A/437G, 385A/437G/478L/547G, 437G, 437G/478L, and 478L, wherein the positions are numbered with reference to SEQ ID NO: 2156.

[0034] In some embodiments, the tyrosine ammonia lyase comprises at least one substitution or substitution sets selected from A4D/T7Q/V57I/Q111K, A4D/T7Q/Q111K/P114S/T437G/T547G, A4D/H16Q/V385A/M478L, A4D/V57I/Q111K/T437G, T7Q/V385A/T547G, F10G/H16Q/T437G, H16Q, H16Q/Y41Q/V57I/Q111K/V385A/T547G, H16Q/Y41Q/V57I/T437G/M478L, H16Q/Y41Q/T437G, H16Q/V57I, H16Q/A241S/T437G, H16Q/V385A, H16Q/V385A/T437G, H16Q/V385A/M478L/T547G, H16Q/T437G, D20G/V385A/T437G/M478L/T547G, V57I, V57I/Q111K/P114S, V57I/Q111K/M478L/T547G, V57I/T437G, Q111K/P114S/R202L/Y234H/L289Q/D305Q/M313L/V324A/N332K/V336I/M410P/L432Y/T435S/Q464R/A504R/V512I/T519A/D523E/K548S/D549G, Q111K/A241S/T437G/M478L,

Q111K/M478L, A241S, A241S/V385A, A241S/V385A/M478L, A241S/V385A/M478L/T547G, A241S/T437G, V385A, V385A/T437G, V385A/T437G/M478L/T547G, T437G, T437G/M478L, and M478L, wherein the positions are numbered with reference to SEQ ID NO: 2156.

[0035] The present invention also provides the variants provided in Tables 1-1, 2-1, 3-1, 4-1, 5-1, 6-1, 7-1, 8-1, 9-1, 9-2, 10-1, 10-2, 11-1, 12-1, 13-1, 14-1, 15-1, 16-1, and/or 17-1. In some embodiments, the variant comprises at least about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 2. In some embodiments, the recombinant tyrosine lyase variant comprises at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 2. In some additional embodiments, the recombinant tyrosine lyase variant comprises at least 90% sequence identity to at least one of the even numbered sequences in SEQ ID NOS: 10-2290. In some additional embodiments, the polypeptide of the recombinant tyrosine ammonia lyase variant comprises one of the even-numbered sequences of SEQ ID NOS: 10-2290. In some further embodiments, the recombinant tyrosine ammonia lyase comprises a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the polypeptide sequence of SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

[0036] In some additional embodiments, the recombinant tyrosine ammonia lyase provided herein is thermostable. In some further embodiments, the recombinant tyrosine ammonia lyase is resistant to proteolysis. In yet some additional embodiments, the recombinant tyrosine ammonia lyase is resistant to at least one digestive tract protease. In some embodiments, the digestive tract protease is selected from chymotrypsin, trypsin, carboxypeptidases, and elastases. In some further embodiments, the recombinant tyrosine ammonia lyase is acid stable. In some additional embodiments, the recombinant tyrosine ammonia lyase is acid stable and resistant to proteolysis. In yet some additional embodiments, the recombinant tyrosine ammonia lyase is purified. In some further embodiments, the recombinant tyrosine ammonia lyase exhibits at least one improved property selected from: i) enhanced catalytic activity; ii) reduced sensitivity to proteolysis; iii) increased tolerance to acidic pH; iv) reduced aggregation; v) decreased K_m for tyrosine; vi) decreased immunogenicity; or a combination of any of i), ii), iii), iv), v), and/or vi), as compared to a reference sequence. In some embodiments, the reference sequence is selected from SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

[0037] The present invention also provides compositions comprising at least one recombinant tyrosine ammonia lyase provided herein. In some embodiments, the compositions comprise one recombinant tyrosine ammonia lyase provided herein.

[0038] The present invention also provides recombinant polynucleotide sequences encoding at least one recombinant tyrosine ammonia lyase provided herein. In some embodiment, a recombinant polynucleotide sequence encodes one recombinant tyrosine ammonia lyase. In some embodiments, the polynucleotide sequence is codon-optimized. In some additional embodiments, the polynucleotide

comprises at least 90% sequence identity to at least one of the odd-numbered sequences of SEQ ID NOS: 9-2289. In yet some further embodiments, the recombinant polynucleotide sequence comprises an odd-numbered sequence of SEQ ID NOS: 9-2289.

[0039] The present invention also provides expression vectors comprising at least one recombinant polynucleotide sequence encoding a recombinant tyrosine ammonia lyase provided herein. In some embodiments, the expression vectors comprises a recombinant polynucleotide sequence encoding a recombinant tyrosine ammonia lyase provided herein. In some embodiments of the expression vectors, the recombinant polynucleotide sequence is operably linked to a control sequence. In some additional embodiments of the expression vectors, the control sequence comprises a promoter. In some additional embodiments of the expression vectors, the control sequence is a promoter. In some embodiments of the expression vectors, the promoter is a heterologous promoter.

[0040] The present invention also provides host cells comprising at least one expression vector provided herein. In some embodiments, the host cell comprises one expression vector provided herein, while in some alternative embodiments, the host cell comprises two or more expression vectors provided herein. In some embodiments, the host cell is prokaryotic, while in some alternative embodiments, the host cell is eukaryotic.

[0041] The present invention also provides methods of producing a recombinant tyrosine ammonia lyase, comprising culturing at least one host cell provided herein, under conditions that the tyrosine ammonia lyase encoded by the recombinant polynucleotide is produced. In some embodiments, the methods further comprise the step of recovering the recombinant tyrosine ammonia lyase. In some additional embodiments, the methods further comprise the step of purifying the recombinant tyrosine ammonia lyase.

[0042] The present invention also provides pharmaceutical compositions for the treatment of tyrosinemia comprising at least one recombinant tyrosine ammonia lyase provided herein. In some embodiments, the pharmaceutical composition further comprises a pharmaceutically acceptable carrier and/or excipient. In some additional embodiments, the pharmaceutical composition is suitable for oral administration to a human. In some embodiments, the pharmaceutical composition is in the form of a pill, tablet, capsule, gelcap, liquid, or emulsion. In yet some further embodiments, the pharmaceutical composition is coadministered with nitisinone. In some additional embodiments, the pharmaceutical composition comprises nitisinone. In some embodiments, the pill, tablet, capsule, or gelcap further comprises an enteric coating. In some additional embodiments, the pharmaceutical composition is suitable for parenteral injection into a human. In yet some additional embodiments, the pharmaceutical composition is coadministered with a phenylalanine ammonia lyase. In some further embodiments, the pharmaceutical composition comprises phenylalanine ammonia lyase. In some embodiments, the pharmaceutical composition comprises a pill, tablet, capsule, or gelcap that further comprises an enteric coating. In yet some additional embodiments, the pharmaceutical composition is coadministered with both nitisinone and a phenylalanine ammonia lyase. In some further

embodiments, the pharmaceutical composition comprises both nitisinone and phenylalanine ammonia lyase. In some embodiments, the pharmaceutical composition comprises a pill, tablet, capsule, or gelcap that further comprises an enteric coating.

[0043] The present invention also provides methods for treating and/or preventing the symptoms of tyrosinemia or alkaptonuria in a subject, comprising providing a subject having tyrosinemia or alkaptonuria, and providing at least one pharmaceutical composition provided herein to the subject. In some embodiments, the methods comprise administering more than one composition or pharmaceutical composition provided herein are administered to the subject. In some alternative embodiments, only one composition or pharmaceutical composition is administered to the subject. In some embodiments, the symptoms of tyrosinemia or alkaptonuria are ameliorated. In yet some further embodiments, the subject is able to eat a diet that is less restricted in its phenylalanine, methionine, and/or tyrosine content than diets required by subjects exhibiting the symptoms of tyrosinemia or alkaptonuria. In some embodiments, the subject is an infant or child, while in some alternative embodiments, the subject is an adult or young adult.

[0044] The present invention also provides methods for the production of L-tyrosine and/or L-tyrosine derivatives comprising the steps of providing at least one recombinant tyrosine ammonia lyase(s) provided herein and a suitable substrate, and combining the recombinant tyrosine ammonia lyase(s) and the substrate under conditions such that L-tyrosine and/or at least one L-tyrosine derivative is produced. In some embodiments, only one recombinant tyrosine ammonia lyase is utilized in the methods, while in some alternative embodiments, at least two recombinant tyrosine ammonia lyases are utilized.

[0045] The present invention also provides methods for the production of coumaric acid, comprising the steps of providing at least one recombinant tyrosine ammonia lyase, and a suitable substrate, and combining the recombinant tyrosine ammonia lyase(s) and the substrate under conditions such that coumaric acid is produced. In some embodiments, only one recombinant tyrosine ammonia lyase is utilized in the methods, while in some alternative embodiments, at least two recombinant tyrosine ammonia lyases are utilized.

[0046] The present invention also provides use of the compositions and pharmaceutical compositions provided herein.

DESCRIPTION OF THE INVENTION

[0047] The present invention provides engineered tyrosine ammonia-lyase (TAL) polypeptides and compositions thereof. In some embodiments, the engineered TAL polypeptides have been optimized to provide enhanced catalytic activity and enhanced acid stability, while reducing sensitivity to proteolysis. The invention also provides methods for utilization of the compositions comprising the engineered TAL polypeptides for therapeutic and industrial purposes.

Abbreviations and Definitions:

[0048] Unless defined otherwise, all technical and scientific terms used herein generally have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Generally, the nomenclature used herein and the laboratory procedures of cell culture, molecular genetics, microbiology, organic chemistry, analytical chemistry and nucleic acid chemistry described below are those well-known and commonly employed in the art. Such techniques are well-known and described in numerous texts and reference works well known to those of skill in the art. Standard techniques, or modifications thereof, are used for chemical syntheses and chemical analyses. All patents, patent applications, articles and publications mentioned herein, both *supra* and *infra*, are hereby expressly incorporated herein by reference.

[0049] Although any suitable methods and materials similar or equivalent to those described herein find use in the practice of the present invention, some methods and materials are described herein. It is to be understood that this invention is not limited to the particular methodology, protocols, and reagents described, as these may vary, depending upon the context they are used by those of skill in the art. Accordingly, the terms defined immediately below are more fully described by reference to the application as a whole. All patents, patent applications, articles and publications mentioned herein, both *supra* and *infra*, are hereby expressly incorporated herein by reference.

[0050] Also, as used herein, the singular "a", "an," and "the" include the plural references, unless the context clearly indicates otherwise.

[0051] Numeric ranges are inclusive of the numbers defining the range. Thus, every numerical range disclosed herein is intended to encompass every narrower numerical range that falls within such broader numerical range, as if such narrower numerical ranges were all expressly written herein. It is also intended that every maximum (or minimum) numerical limitation disclosed herein includes every lower (or higher) numerical limitation, as if such lower (or higher) numerical limitations were expressly written herein.

[0052] The term "about" means an acceptable error for a particular value. In some instances "about" means within 0.05%, 0.5%, 1.0%, or 2.0%, of a given value range. In some instances, "about" means within 1, 2, 3, or 4 standard deviations of a given value. In some instances, "about" encompasses values that are within 2.5%, 3%, 3.5%, 4%, 4.5%, 5%, 5.5%, 6%, 6.5%, 7%, 7.5%, 8%, 8.5%, 9%, 9.5%, or 10% of a given value.

[0053] Furthermore, the headings provided herein are not limitations of the various aspects or embodiments of the invention which can be had by reference to the application as a whole. Accordingly, the terms defined immediately below are more fully defined by reference to the application as a whole. Nonetheless, in order to facilitate understanding of the invention, a number of terms are defined below.

[0054] Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxy orientation, respectively.

[0055] As used herein, the term “comprising” and its cognates are used in their inclusive sense (*i.e.*, equivalent to the term “including” and its corresponding cognates).

[0056] “EC” number refers to the Enzyme Nomenclature of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (NC-IUBMB). The IUBMB biochemical classification is a numerical classification system for enzymes based on the chemical reactions they catalyze.

[0057] “ATCC” refers to the American Type Culture Collection whose biorepository collection includes genes and strains.

[0058] “NCBI” refers to National Center for Biological Information and the sequence databases provided therein.

[0059] As used herein, the terms “tyrosine ammonia-lyase” “tyrosine ammonia lyase,” “tyrosine ammonia lyase polypeptide” and “TAL” refer to a class of enzymes within the aromatic amino acid lyase family (EC 4.3.1.23, EC 4.3.1.24 and EC4.3.1.25) which also includes histidine ammonia-lyase, and phenylalanine ammonia-lyase.

[0060] “Protein,” “polypeptide,” and “peptide” are used interchangeably herein to denote a polymer of at least two amino acids covalently linked by an amide bond, regardless of length or post-translational modification (e.g., glycosylation or phosphorylation).

[0061] “Amino acids” are referred to herein by either their commonly known three-letter symbols or by the one-letter symbols recommended by IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single letter codes. “Amino acids” are referred to herein by either their commonly known three-letter symbols or by the one-letter symbols recommended by IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single letter codes. The abbreviations used for the genetically encoded amino acids are conventional and are as follows: alanine (Ala or A), arginine (Arg or R), asparagine (Asn or N), aspartate (Asp or D), cysteine (Cys or C), glutamate (Glu or E), glutamine (Gln or Q), histidine (His or H), isoleucine (Ile or I), leucine (Leu or L), lysine (Lys or K), methionine (Met or M), phenylalanine (Phe or F), proline (Pro or P), serine (Ser or S), threonine (Thr or T), tryptophan (Trp or W), tyrosine (Tyr or Y), and valine (Val or V). When the three-letter abbreviations are used, unless specifically preceded by an “L” or a “D” or clear from the context in which the abbreviation is used, the amino acid may be in either the L- or D-configuration about α -carbon (C_α). For example, whereas “Ala” designates alanine without specifying the configuration about the α -carbon, “D-Ala” and “L-Ala” designate D-alanine and L-alanine, respectively. When the one-letter abbreviations are used, upper case letters designate amino acids in the L-configuration about the α -carbon and lower case letters designate amino acids in the D-

configuration about the α -carbon. For example, “A” designates L-alanine and “a” designates D-alanine. When polypeptide sequences are presented as a string of one-letter or three-letter abbreviations (or mixtures thereof), the sequences are presented in the amino (N) to carboxy (C) direction in accordance with common convention.

[0062] The abbreviations used for the genetically encoding nucleosides are conventional and are as follows: adenosine (A); guanosine (G); cytidine (C); thymidine (T); and uridine (U). Unless specifically delineated, the abbreviated nucleosides may be either ribonucleosides or 2'-deoxyribonucleosides. The nucleosides may be specified as being either ribonucleosides or 2'-deoxyribonucleosides on an individual basis or on an aggregate basis. When nucleic acid sequences are presented as a string of one-letter abbreviations, the sequences are presented in the 5' to 3' direction in accordance with common convention, and the phosphates are not indicated.

[0063] The term “engineered,” “recombinant,” “non-naturally occurring,” and “variant,” when used with reference to a cell, a polynucleotide or a polypeptide refers to a material or a material corresponding to the natural or native form of the material that has been modified in a manner that would not otherwise exist in nature or is identical thereto but produced or derived from synthetic materials and/or by manipulation using recombinant techniques.

[0064] As used herein, “wild-type” and “naturally-occurring” refer to the form found in nature. For example a wild-type polypeptide or polynucleotide sequence is a sequence present in an organism that can be isolated from a source in nature and which has not been intentionally modified by human manipulation.

[0065] “Deimmunized” as used herein, refers to the manipulation of a protein to create a variant that is not as immunogenic as the wild-type or reference protein. In some embodiments, the deimmunization is complete, in that the variant protein does not stimulate an immune response in patients to whom the variant protein is administered. This response can be measured by various methods including but not limited to, the presence or abundance of anti-drug antibodies, the presence or abundance of neutralizing antibodies, the presence of an anaphylactic response, or the prevalence or intensity of cytokine release upon administration of the protein. In some embodiments, the variant protein is less immunogenic than the wild-type or reference protein. In some embodiments, deimmunization involves modifications to proteins (e.g., epitopes) that are recognized by T-cell receptors. In some embodiments, the T-cell epitopes are removed from a wild-type or reference protein in order to produce a deimmunized variant protein. In some embodiments, the deimmunized protein shows lower levels of response in biochemical and cell-biological predictors of human immunological responses including dendritic-cell T-cell activation assays, or human leukocyte antigen (HLA) peptide binding assays.

[0066] “Coding sequence” refers to that part of a nucleic acid (e.g., a gene) that encodes an amino acid sequence of a protein.

[0067] The term “percent (%) sequence identity” is used herein to refer to comparisons among polynucleotides and polypeptides, and are determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence for optimal alignment of the two sequences. The percentage may be calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Alternatively, the percentage may be calculated by determining the number of positions at which either the identical nucleic acid base or amino acid residue occurs in both sequences or a nucleic acid base or amino acid residue is aligned with a gap to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Those of skill in the art appreciate that there are many established algorithms available to align two sequences. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (Smith and Waterman, *Adv. Appl. Math.*, 2:482 [1981]), by the homology alignment algorithm of Needleman and Wunsch (Needleman and Wunsch, *J. Mol. Biol.*, 48:443 [1970]), by the search for similarity method of Pearson and Lipman (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444 [1988]), by computerized implementations of these algorithms (e.g., GAP, BESTFIT, FASTA, and TFASTA in the GCG Wisconsin Software Package), or by visual inspection, as known in the art. Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include, but are not limited to the BLAST and BLAST 2.0 algorithms, which are described by Altschul et al. (See, Altschul et al., *J. Mol. Biol.*, 215: 403-410 [1990]; and Altschul et al., 1977, *Nucleic Acids Res.*, 3389-3402 [1977], respectively). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information website. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as, the neighborhood word score threshold (See, Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring

residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (See, Henikoff and Henikoff, Proc. Natl. Acad. Sci. USA 89:10915 [1989]). Exemplary determination of sequence alignment and % sequence identity can employ the BESTFIT or GAP programs in the GCG Wisconsin Software package (Accelrys, Madison WI), using default parameters provided.

[0068] “Reference sequence” refers to a defined sequence used as a basis for a sequence comparison. A reference sequence may be a subset of a larger sequence, for example, a segment of a full-length gene or polypeptide sequence. Generally, a reference sequence is at least 20 nucleotide or amino acid residues in length, at least 25 residues in length, at least 50 residues in length, at least 100 residues in length or the full length of the nucleic acid or polypeptide. Since two polynucleotides or polypeptides may each (1) comprise a sequence (*i.e.*, a portion of the complete sequence) that is similar between the two sequences, and (2) may further comprise a sequence that is divergent between the two sequences, sequence comparisons between two (or more) polynucleotides or polypeptide are typically performed by comparing sequences of the two polynucleotides or polypeptides over a “comparison window” to identify and compare local regions of sequence similarity. In some embodiments, a “reference sequence” can be based on a primary amino acid sequence, where the reference sequence is a sequence that can have one or more changes in the primary sequence.

[0069] “Comparison window” refers to a conceptual segment of at least about 20 contiguous nucleotide positions or amino acids residues wherein a sequence may be compared to a reference sequence of at least 20 contiguous nucleotides or amino acids and wherein the portion of the sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The comparison window can be longer than 20 contiguous residues, and includes, optionally 30, 40, 50, 100, or longer windows.

[0070] “Corresponding to”, “reference to” or “relative to” when used in the context of the numbering of a given amino acid or polynucleotide sequence refers to the numbering of the residues of a specified reference sequence when the given amino acid or polynucleotide sequence is compared to the reference sequence. In other words, the residue number or residue position of a given polymer is designated with respect to the reference sequence rather than by the actual numerical position of the residue within the given amino acid or polynucleotide sequence. For example, a given amino acid sequence, such as that of an engineered TAL, can be aligned to a reference sequence by introducing gaps to optimize residue matches between the two sequences. In these cases, although the gaps are present, the numbering of the residue in the given amino acid or polynucleotide sequence is made with respect to the reference sequence to which it has been aligned.

[0071] “Amino acid difference” or “residue difference” refers to a difference in the amino acid residue at a position of a polypeptide sequence relative to the amino acid residue at a corresponding position in a reference sequence. The positions of amino acid differences generally are referred to herein as “X_n,” where n refers to the corresponding position in the reference sequence upon which the residue difference is based. For example, a “residue difference at position X93 as compared to SEQ ID NO: 2” refers to a difference of the amino acid residue at the polypeptide position corresponding to position 93 of SEQ ID NO: 2. Thus, if the reference polypeptide of SEQ ID NO: 2 has a leucine at position 93, then a “residue difference at position X93 as compared to SEQ ID NO: 2” has an amino acid substitution of any residue other than leucine at the position of the polypeptide corresponding to position 93 of SEQ ID NO: 2. In most instances herein, the specific amino acid residue difference at a position is indicated as “X_nY” where “X_n” specified the corresponding position as described above, and “Y” is the single letter identifier of the amino acid found in the engineered polypeptide (i.e., the different residue than in the reference polypeptide). In some instances, the present disclosure also provides specific amino acid differences denoted by the conventional notation “A_nB”, where A is the single letter identifier of the residue in the reference sequence, “n” is the number of the residue position in the reference sequence, and B is the single letter identifier of the residue substitution in the sequence of the engineered polypeptide. In some instances, a polypeptide of the present disclosure can include one or more amino acid residue differences relative to a reference sequence, which is indicated by a list of the specified positions where residue differences are present relative to the reference sequence. In some embodiments, where more than one amino acid can be used in a specific residue position of a polypeptide, the various amino acid residues that can be used are separated by a “/” (e.g., X307H/X307P or X307H/P). The present application includes engineered polypeptide sequences comprising one or more amino acid differences that include either/or both conservative and non-conservative amino acid substitutions.

[0072] “Conservative amino acid substitution” refers to a substitution of a residue with a different residue having a similar side chain, and thus typically involves substitution of the amino acid in the polypeptide with amino acids within the same or similar defined class of amino acids. By way of example and not limitation, an amino acid with an aliphatic side chain may be substituted with another aliphatic amino acid (e.g., alanine, valine, leucine, and isoleucine); an amino acid with hydroxyl side chain is substituted with another amino acid with a hydroxyl side chain (e.g., serine and threonine); an amino acids having aromatic side chains is substituted with another amino acid having an aromatic side chain (e.g., phenylalanine, tyrosine, tryptophan, and histidine); an amino acid with a basic side chain is substituted with another amino acid with a basis side chain (e.g., lysine and arginine); an amino acid with an acidic side chain is substituted with another amino acid with an acidic side chain (e.g., aspartic acid or glutamic acid); and/or a hydrophobic or hydrophilic amino acid is replaced with another hydrophobic or hydrophilic amino acid, respectively.

[0073] “Non-conservative substitution” refers to substitution of an amino acid in the polypeptide with an amino acid with significantly differing side chain properties. Non-conservative substitutions may use amino acids between, rather than within, the defined groups and affects (a) the structure of the peptide backbone in the area of the substitution (e.g., proline for glycine) (b) the charge or hydrophobicity, or (c) the bulk of the side chain. By way of example and not limitation, an exemplary non-conservative substitution can be an acidic amino acid substituted with a basic or aliphatic amino acid; an aromatic amino acid substituted with a small amino acid; and a hydrophilic amino acid substituted with a hydrophobic amino acid.

[0074] “Deletion” refers to modification to the polypeptide by removal of one or more amino acids from the reference polypeptide. Deletions can comprise removal of 1 or more amino acids, 2 or more amino acids, 5 or more amino acids, 10 or more amino acids, 15 or more amino acids, or 20 or more amino acids, up to 10% of the total number of amino acids, or up to 20% of the total number of amino acids making up the reference enzyme while retaining enzymatic activity and/or retaining the improved properties of an engineered transaminase enzyme. Deletions can be directed to the internal portions and/or terminal portions of the polypeptide. In various embodiments, the deletion can comprise a continuous segment or can be discontinuous.

[0075] “Insertion” refers to modification to the polypeptide by addition of one or more amino acids from the reference polypeptide. Insertions can be in the internal portions of the polypeptide, or to the carboxy or amino terminus. Insertions as used herein include fusion proteins as is known in the art. The insertion can be a contiguous segment of amino acids or separated by one or more of the amino acids in the naturally occurring polypeptide.

[0076] A “functional fragment” or a “biologically active fragment” used interchangeably herein refers to a polypeptide that has an amino-terminal and/or carboxy-terminal deletion(s) and/or internal deletions, but where the remaining amino acid sequence is identical to the corresponding positions in the sequence to which it is being compared (e.g., a full-length engineered TAL of the present invention) and that retains substantially all of the activity of the full-length polypeptide.

[0077] “Isolated polypeptide” refers to a polypeptide which is substantially separated from other contaminants that naturally accompany it (e.g., protein, lipids, and polynucleotides). The term embraces polypeptides which have been removed or purified from their naturally-occurring environment or expression system (e.g., host cell or *in vitro* synthesis). The recombinant TAL polypeptides may be present within a cell, present in the cellular medium, or prepared in various forms, such as lysates or isolated preparations. As such, in some embodiments, the recombinant TAL polypeptides can be an isolated polypeptide.

[0078] “Substantially pure polypeptide” refers to a composition in which the polypeptide species is the predominant species present (i.e., on a molar or weight basis it is more abundant than any other individual macromolecular species in the composition), and is generally a substantially purified composition when the object species comprises at least about 50 percent of the macromolecular

species present by mole or % weight. Generally, a substantially pure TAL composition comprises about 60% or more, about 70% or more, about 80% or more, about 90% or more, about 95% or more, and about 98% or more of all macromolecular species by mole or % weight present in the composition. In some embodiments, the object species is purified to essential homogeneity (i.e., contaminant species cannot be detected in the composition by conventional detection methods) wherein the composition consists essentially of a single macromolecular species. Solvent species, small molecules (<500 Daltons), and elemental ion species are not considered macromolecular species. In some embodiments, the isolated recombinant TAL polypeptides are substantially pure polypeptide compositions.

[0079] “Improved enzyme property” refers to an engineered TAL polypeptide that exhibits an improvement in any enzyme property as compared to a reference TAL polypeptide and/or as a wild-type PAL polypeptide (e.g., the wild-type sequence of SEQ ID NO: 2) or another engineered TAL polypeptide. Improved properties include but are not limited to such properties as increased protein expression, increased thermoactivity, increased thermostability, increased pH activity, increased stability, increased enzymatic activity, increased substrate specificity or affinity, increased specific activity, increased resistance to substrate or end-product inhibition, increased chemical stability, improved chemoselectivity, improved solvent stability, increased tolerance to acidic pH, increased tolerance to proteolytic activity (i.e., reduced sensitivity to proteolysis), reduced aggregation, increased solubility, reduced immunogenicity, and altered temperature profile.

[0080] “Increased enzymatic activity” or “enhanced catalytic activity” refers to an improved property of the engineered TAL polypeptides, which can be represented by an increase in specific activity (e.g., product produced/time/weight protein) or an increase in percent conversion of the substrate to the product (e.g., percent conversion of starting amount of substrate to product in a specified time period using a specified amount of TAL) as compared to the reference TAL enzyme. Exemplary methods to determine enzyme activity are provided in the Examples. Any property relating to enzyme activity may be affected, including the classical enzyme properties of K_m , V_{max} or k_{cat} , changes of which can lead to increased enzymatic activity. Improvements in enzyme activity can be from about 1.1 fold the enzymatic activity of the corresponding wild-type enzyme, to as much as 2-fold, 5-fold, 10-fold, 20-fold, 25-fold, 50-fold, 75-fold, 100-fold, 150-fold, 200-fold or more enzymatic activity than the naturally occurring TAL or another engineered TAL from which the TAL polypeptides were derived.

[0081] In some embodiments, the engineered TAL polypeptides have a k_{cat} of at least 0.1/sec, at least 0.2/sec, at least 0.3/sec, at least 0.5/sec, at least 1.0/sec and in some preferred embodiments greater than 1.0/sec. In some embodiments, the K_m is in the range of about 1 μ M to about 5mM; in the range of about 5 μ M to about 2mM; in the range of about 10 μ M to about 2mM; or in the range of about 10 μ M to about 1mM. In some specific embodiments, the engineered TAL enzyme exhibits improved enzymatic activity in the range of 1.5 to 10 fold, 1.5 to 25 fold, 1.5 to 50 fold, 1.5 to 100 fold or greater than that of a reference TAL enzyme (e.g., a wild-type TAL or any other reference TAL).

TAL activity can be measured by any suitable method known in the art (e.g., standard assays, such as monitoring changes in spectrophotometric properties of reactants or products). In some embodiments, the amount of products produced can be measured by High-Performance Liquid Chromatography (HPLC) separation combined with UV absorbance or fluorescent detection directly or following o-phthalaldehyde (OPA) derivatization. In some embodiments, other methods are used, such as tracking the coumarate product (e.g., use UV absorbance to track its production at 290 nm or 310 nm). In some other embodiments, the production of ammonia is assayed using commercially available kits (e.g., the Megazyme rapid ammonia assay kit [Megazyme International, Wicklow, Ireland]). Comparisons of enzyme activities are made using a defined preparation of enzyme, a defined assay under a set condition, and one or more defined substrates, as further described in detail herein. Generally, when lysates are compared, the numbers of cells and the amount of protein assayed are determined as well as use of identical expression systems and identical host cells to minimize variations in amount of enzyme produced by the host cells and present in the lysates.

[0082] The terms "thermally stable" and "thermostable" refer to enzymes of the present invention that retain a specified amount of enzymatic activity, primary, secondary, tertiary and quaternary structure after exposure to identified temperatures over a given period of time under conditions prevailing during the use of the enzyme, for example, when exposed to altered temperatures. "Altered temperatures" include increased or decreased temperatures. In some embodiments, the enzymes retain at least about 50%, about 60%, about 70%, about 75%, about 80%, about 85%, about 90%, about 92%, about 95%, about 96%, about 97%, about 98%, or about 99% enzymatic activity after exposure to altered temperatures over a given time period, for example, at least about 60 minutes, about 120 minutes, about 180 minutes, about 240 minutes, about 300 minutes, etc.

[0083] The term "improved tolerance to acidic pH" means that a recombinant TAL according to the invention will have increased stability (higher retained activity at about pH 7.0 after exposure to acidic pH for a specified period of time (1 hour, up to 24 hours)) as compared to a reference TAL or another enzyme.

[0084] "Physiological pH" as used herein means the pH range generally found in a subject's (e.g., human) small intestine. There normally is a pH gradient from the pyloric sphincter to the large intestine from about 5.0 to 7.5.

[0085] The term "acidic pH" (e.g., used with reference to improved stability to acidic pH conditions or increased tolerance to acidic pH) means a pH range of about 1.5 to 6.8.

[0086] The terms "proteolytic activity" and "proteolysis" used interchangeably herein refer to the breakdown of proteins into smaller polypeptides or amino acids. The breakdown of proteins is generally the result of hydrolysis of the peptide bond by protease (proteinase) enzymes. Protease enzymes include but are not limited to pepsin, trypsin, chymotrypsin, elastase, carboxypeptidase A and B, peptidases (e.g., amino peptidase, dipeptidase and enteropeptidase).

[0087] The phrases “reducing sensitivity to proteolysis” and “reducing proteolytic sensitivity” used interchangeably herein mean that an engineered TAL polypeptide according to the invention will have a higher enzyme activity compared to a reference TAL and/or another enzyme in a standard assay after treatment with one or more proteases. Exemplary assays are provided in the Examples.

[0088] “Aggregation” means clumping or precipitation of a TAL polypeptide. Aggregation can lead to inactivation, and/or increased immunogenicity of the enzyme. The term “reduced aggregation” means an engineered TAL polypeptide will be less prone to aggregation or to aggregate than a reference TAL and/or another enzyme. Methods for determining Aggregation can be determined by one of general skill in the art by using any number of assays including but not limited to fluorescent microscopy with appropriate dyes (e.g., thioflavin T or Nile Red), dynamic light scattering, flow cytometry with appropriate dyes (e.g. Bodipy), filtration and analysis by SDS-PAGE or Western blotting, fluorescent correlation spectroscopy, and electron microscopy. There are commercially available kits to assess aggregation (e.g., the PROTEOSTAT[®] Protein Aggregation Assay kit [Enzo]).

[0089] “Conversion” refers to the enzymatic conversion (or biotransformation) of a substrate(s) to the corresponding product(s). “Percent conversion” refers to the percent of the substrate that is converted to the product within a period of time under specified conditions. Thus, the “enzymatic activity” or “activity” of a TAL polypeptide can be expressed as “percent conversion” of the substrate to the product in a specific period of time.

[0090] “Hybridization stringency” relates to hybridization conditions, such as washing conditions, in the hybridization of nucleic acids. Generally, hybridization reactions are performed under conditions of lower stringency, followed by washes of varying but higher stringency. The term “moderately stringent hybridization” refers to conditions that permit target-DNA to bind a complementary nucleic acid that has about 60% identity, preferably about 75% identity, about 85% identity to the target DNA, with greater than about 90% identity to target-polynucleotide. Exemplary moderately stringent conditions are conditions equivalent to hybridization in 50% formamide, 5× Denhart's solution, 5×SSPE, 0.2% SDS at 42°C, followed by washing in 0.2×SSPE, 0.2% SDS, at 42°C. “High stringency hybridization” refers generally to conditions that are about 10°C or less from the thermal melting temperature T_m as determined under the solution condition for a defined polynucleotide sequence. In some embodiments, a high stringency condition refers to conditions that permit hybridization of only those nucleic acid sequences that form stable hybrids in 0.018M NaCl at 65°C (i.e., if a hybrid is not stable in 0.018M NaCl at 65°C, it will not be stable under high stringency conditions, as contemplated herein). High stringency conditions can be provided, for example, by hybridization in conditions equivalent to 50% formamide, 5× Denhart's solution, 5×SSPE, 0.2% SDS at 42°C, followed by washing in 0.1×SSPE, and 0.1% SDS at 65°C. Another high stringency condition is hybridizing in conditions equivalent to hybridizing in 5X SSC containing 0.1% (w:v) SDS at 65°C and washing in 0.1x SSC containing 0.1% SDS at 65°C. Other high stringency

hybridization conditions, as well as moderately stringent conditions, are described in the references cited above.

[0091] “Codon optimized” refers to changes in the codons of the polynucleotide encoding a protein to those preferentially used in a particular organism such that the encoded protein is more efficiently expressed in the organism of interest. Although the genetic code is degenerate in that most amino acids are represented by several codons, called “synonyms” or “synonymous” codons, it is well known that codon usage by particular organisms is nonrandom and biased towards particular codon triplets. This codon usage bias may be higher in reference to a given gene, genes of common function or ancestral origin, highly expressed proteins versus low copy number proteins, and the aggregate protein coding regions of an organism's genome. In some embodiments, the polynucleotides encoding the TAL enzymes may be codon optimized for optimal production from the host organism selected for expression.

[0092] “Control sequence” refers herein to include all components, which are necessary or advantageous for the expression of a polynucleotide and/or polypeptide of the present application. Each control sequence may be native or foreign to the nucleic acid sequence encoding the polypeptide. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter sequence, signal peptide sequence, initiation sequence and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the nucleic acid sequence encoding a polypeptide.

[0093] “Operably linked” is defined herein as a configuration in which a control sequence is appropriately placed (i.e., in a functional relationship) at a position relative to a polynucleotide of interest such that the control sequence directs or regulates the expression of the polynucleotide and/or polypeptide of interest.

[0094] “Promoter sequence” refers to a nucleic acid sequence that is recognized by a host cell for expression of a polynucleotide of interest, such as a coding sequence. The promoter sequence contains transcriptional control sequences, which mediate the expression of a polynucleotide of interest. The promoter may be any nucleic acid sequence which shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

[0095] “Suitable reaction conditions” refers to those conditions in the enzymatic conversion reaction solution (e.g., ranges of enzyme loading, substrate loading, temperature, pH, buffers, co-solvents, etc.) under which a TAL polypeptide of the present application is capable of converting a substrate to the desired product compound. Exemplary “suitable reaction conditions” are provided in the present application and illustrated by the Examples. “Loading”, such as in “compound loading” or “enzyme loading” refers to the concentration or amount of a component in a reaction mixture at the start of the

reaction. "Substrate" in the context of an enzymatic conversion reaction process refers to the compound or molecule acted on by the TAL polypeptide. "Product" in the context of an enzymatic conversion process refers to the compound or molecule resulting from the action of the TAL polypeptide on a substrate.

[0096] As used herein the term "culturing" refers to the growing of a population of microbial cells under any suitable conditions (e.g., using a liquid, gel or solid medium).

[0097] Recombinant polypeptides can be produced using any suitable methods known the art. Genes encoding the wild-type polypeptide of interest can be cloned in vectors, such as plasmids, and expressed in desired hosts, such as *E. coli*, etc. Variants of recombinant polypeptides can be generated by various methods known in the art. Indeed, there is a wide variety of different mutagenesis techniques well known to those skilled in the art. In addition, mutagenesis kits are also available from many commercial molecular biology suppliers. Methods are available to make specific substitutions at defined amino acids (site-directed), specific or random mutations in a localized region of the gene (regio-specific), or random mutagenesis over the entire gene (e.g., saturation mutagenesis).

Numerous suitable methods are known to those in the art to generate enzyme variants, including but not limited to site-directed mutagenesis of single-stranded DNA or double-stranded DNA using PCR, cassette mutagenesis, gene synthesis, error-prone PCR, shuffling, and chemical saturation mutagenesis, or any other suitable method known in the art. Non-limiting examples of methods used for DNA and protein engineering are provided in the following patents: US Pat. No. 6,117,679; US Pat. No. 6,420,175; US Pat. No. 6,376,246; US Pat. No. 6,586,182; US Pat. No. 7,747,391; US Pat. No. 7,747,393; US Pat. No. 7,783,428; and US Pat. No. 8,383,346. After the variants are produced, they can be screened for any desired property (e.g., high or increased activity, or low or reduced activity, increased thermal activity, increased thermal stability, and/or acidic pH stability, etc.). In some embodiments, "recombinant TAL polypeptides" (also referred to herein as "engineered TAL polypeptides," "variant TAL enzymes," and "TAL variants") find use.

[0098] As used herein, a "vector" is a DNA construct for introducing a DNA sequence into a cell. In some embodiments, the vector is an expression vector that is operably linked to a suitable control sequence capable of effecting the expression in a suitable host of the polypeptide encoded in the DNA sequence. In some embodiments, an "expression vector" has a promoter sequence operably linked to the DNA sequence (e.g., transgene) to drive expression in a host cell, and in some embodiments, also comprises a transcription terminator sequence.

[0099] As used herein, the term "expression" includes any step involved in the production of the polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, and post-translational modification. In some embodiments, the term also encompasses secretion of the polypeptide from a cell.

[0100] As used herein, the term "produces" refers to the production of proteins and/or other compounds by cells. It is intended that the term encompass any step involved in the production of

polypeptides including, but not limited to, transcription, post-transcriptional modification, translation, and post-translational modification. In some embodiments, the term also encompasses secretion of the polypeptide from a cell.

[0101] As used herein, an amino acid or nucleotide sequence (*e.g.*, a promoter sequence, signal peptide, terminator sequence, etc.) is "heterologous" to another sequence with which it is operably linked if the two sequences are not associated in nature.

[0102] As used herein, the terms "host cell" and "host strain" refer to suitable hosts for expression vectors comprising DNA provided herein (*e.g.*, the polynucleotides encoding the TAL variants). In some embodiments, the host cells are prokaryotic or eukaryotic cells that have been transformed or transfected with vectors constructed using recombinant DNA techniques as known in the art.

[0103] The term "analogue" means a polypeptide having more than 70% sequence identity but less than 100% sequence identity (*e.g.*, more than 75%, 78%, 80%, 83%, 85%, 88%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity) with a reference polypeptide. In some embodiments, analogues means polypeptides that contain one or more non-naturally occurring amino acid residues including, but not limited, to homoarginine, ornithine and norvaline, as well as naturally occurring amino acids. In some embodiments, analogues also include one or more D-amino acid residues and non-peptide linkages between two or more amino acid residues.

[0104] The term "therapeutic" refers to a compound administered to a subject who shows signs or symptoms of pathology having beneficial or desirable medical effects.

[0105] The term "pharmaceutical composition" refers to a composition suitable for pharmaceutical use in a mammalian subject (*e.g.*, human) comprising a pharmaceutically effective amount of an engineered TAL polypeptide encompassed by the invention and an acceptable carrier.

[0106] The term "effective amount" means an amount sufficient to produce the desired result. One of general skill in the art may determine what the effective amount by using routine experimentation.

[0107] The terms "isolated" and "purified" are used to refer to a molecule (*e.g.*, an isolated nucleic acid, polypeptide, etc.) or other component that is removed from at least one other component with which it is naturally associated. The term "purified" does not require absolute purity, rather it is intended as a relative definition.

[0108] The term "subject" encompasses mammals such as humans, non-human primates, livestock, companion animals, and laboratory animals (*e.g.*, rodents and lagamorphs). It is intended that the term encompass females as well as males.

[0109] As used herein, the term "patient" means any subject that is being assessed for, treated for, or is experiencing disease.

[0110] The term "infant" refers to a child in the period of the first month after birth to approximately one (1) year of age. As used herein, the term "newborn" refers to child in the period from birth to the 28th day of life. The term "premature infant" refers to an infant born after the twentieth completed

week of gestation, yet before full term, generally weighing ~500 to ~2499 grams at birth. A “very low birth weight infant” is an infant weighing less than 1500 g at birth.

[0111] As used herein, the term “child” refers to a person who has not attained the legal age for consent to treatment or research procedures. In some embodiments, the term refers to a person between the time of birth and adolescence.

[0112] As used herein, the term “adult” refers to a person who has attained legal age for the relevant jurisdiction (e.g., 18 years of age in the United States). In some embodiments, the term refers to any fully grown, mature organism. In some embodiments, the term “young adult” refers to a person less than 18 years of age, but who has reached sexual maturity.

[0113] As used herein, “composition” and “formulation” encompass products comprising at least one engineered TAL of the present invention, intended for any suitable use (e.g., pharmaceutical compositions, dietary/nutritional supplements, feed, etc.).

[0114] The terms “administration” and “administering” a composition mean providing a composition of the present invention to a subject (e.g., to a person suffering from the effects of tyrosinemia or alkaptonuria).

[0115] The term “carrier” when used in reference to a pharmaceutical composition means any of the standard pharmaceutical carrier, buffers, and excipients, such as stabilizers, preservatives, and adjuvants.

[0116] The term “pharmaceutically acceptable” means a material that can be administered to a subject without causing any undesirable biological effects or interacting in a deleterious manner with any of the components in which it is contained and that possesses the desired biological activity.

[0117] As used herein, the term “excipient” refers to any pharmaceutically acceptable additive, carrier, diluent, adjuvant, or other ingredient, other than the active pharmaceutical ingredient (API; e.g., the engineered TAL polypeptides of the present invention). Excipients are typically included for formulation and/or administration purposes.

[0118] The term “therapeutically effective amount” when used in reference to symptoms of disease/condition refers to the amount and/or concentration of a compound (e.g., engineered TAL polypeptides) that ameliorates, attenuates, or eliminates one or more symptom of a disease/condition or prevents or delays the onset of symptom(s).

[0119] The term “therapeutically effective amount” when used in reference to a disease/condition refers to the amount and/or concentration of a composition (e.g., engineered TAL polypeptides) that ameliorates, attenuates, or eliminates the disease/condition. In some embodiments, the term is use in reference to the amount of a composition that elicits the biological (e.g., medical) response by a tissue, system, or animal subject that is sought by the researcher, physician, veterinarian, or other clinician.

[0120] It is intended that the terms “treating,” “treat” and “treatment” encompass preventative (e.g., prophylactic), as well as palliative treatment.

Engineered TAL Polypeptides:

[0121] The parent enzyme used to generate the engineered TAL polypeptides is selected from enzymes obtained from *Stanieria cyanosphaera* (SEQ ID NO: 2), *Chroogloeocystis siderophila* (SEQ ID NO: 4), *Flavobacterium johnsoniae* (SEQ ID NO: 6), and *Rhodotorula glutinis* (SEQ ID NO: 8). In some embodiments, the engineered TAL polypeptides are derived by directed evolution from *S. cyanosphaera*. Furthermore, when a particular TAL variant (engineered TAL polypeptide) is referred to by reference to modification of particular amino acids residues in the sequence of a wild-type TAL, wild-type PAL, wild-type HAL or another TAL, it is to be understood that variants of another TAL modified in the equivalent position(s) (as determined from the optional amino acid sequence alignment between the respective amino acid sequences) are encompassed herein. In some embodiments the engineered TAL polypeptide will comprise the conserved active site Ala164-Ser165-Gly166 and comprise at least 70% (at least 75%, at least 80%, at least 85%, at least 90%, at least 93%, at least 95%, at least 97%) sequence identity to SEQ ID NO: 2. In some embodiments the engineered TAL polypeptides comprise not only TAL activity but also may be active on phenylalanine and/or histidine substrates. In some embodiments, TAL variants are developed that comprise at least one mutation in at least one key residue (See e.g., WO 2008/069958; US Appln. Ser. No. 2009/011140; and Watts et al. Chem. Biol., 13:1317-26 [2006]).

[0122] In some embodiments, engineered TAL polypeptides are produced by cultivating a microorganism comprising at least one polynucleotide sequence encoding at least one engineered TAL polypeptide under conditions which are conducive for producing the engineered TAL polypeptide(s). In some embodiments, the engineered TAL polypeptide is recovered from the resulting culture medium and/or cells.

[0123] The present invention provides exemplary engineered TAL polypeptides having TAL activity. The Examples provide Tables showing sequence structural information correlating specific amino acid sequence features with the functional activity of the engineered TAL polypeptides. This structure-function correlation information is provided in the form of specific amino acid residues differences relative to a reference engineered polypeptide, as indicated in the Examples. The Examples further provide experimentally determined activity data for the exemplary engineered TAL polypeptides.

[0124] In some embodiments, the engineered TAL polypeptides of the invention having TAL activity comprise a) an amino acid sequence having at least about 85% sequence identity to reference sequence SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156; b) an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions; and c) which exhibits an improved property selected from i) enhanced catalytic activity, ii) reduced proteolytic sensitivity, iii) increased tolerance to acidic pH, iv) reduced aggregation or a combination

of any of i), ii), iii) or iv), as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and/or another reference sequence.

[0125] In some embodiments the engineered TAL which exhibits an improved property has at least about 85%, at least about 88%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at about 100% amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions (e.g., at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 20 or more amino acid positions compared to SEQ ID NO: 2, or a sequence having at least 85%, at least 88%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156). In some embodiment the residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more positions will include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more conservative amino acid substitutions. In some embodiments the engineered TAL which exhibits an improved property has at least 85%, at least 88%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

[0126] In some embodiments, the engineered TAL polypeptides of the invention having TAL activity comprise a) an amino acid sequence having at least 85% sequence identity to reference sequence SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156; b) an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions; and c) which exhibits an improved property selected from i) enhanced catalytic activity, ii) reduced proteolytic sensitivity, iii) increased tolerance to acidic pH, iv) reduced aggregation or a combination of any of i), ii), iii) or iv), as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and/or another reference sequence.

[0127] In some embodiments, the engineered TAL polypeptide is a polypeptide listed in Table 1-1, 2-1, 3-1, 4-1, 5-1, 6-1, 7-1, 8-1, 9-1, 9-2, 10-1, 10-2, 11-1, 12-1, 13-1, 14-1, 15-1, 16-1, and/or 17-1.

[0128] In some embodiments, the engineered TAL polypeptide comprises a functional fragment of an engineered TAL polypeptide encompassed by the invention. Functional fragments have at least 95%, 96%, 97%, 98%, or 99% of the activity of the engineered TAL polypeptide from which is was derived (i.e., the parent engineered TAL). A functional fragment comprises at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% and even 99% of the parent sequence of the engineered TAL. In some embodiments the functional fragment is truncated by less than 5, less than 10, less than 15, less

than 10, less than 25, less than 30, less than 35, less than 40, less than 45, and less than 50 amino acids.

Variants with Reduced Sensitivity to Proteolysis:

[0129] In some embodiments, the engineered TAL polypeptides of the invention having TAL activity comprise a) an amino acid sequence having at least 85% sequence identity to reference sequence SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156; b) an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions; and c) which exhibits reduced sensitivity to proteolysis as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and/or another reference sequence.

[0130] In some embodiments the engineered TAL which exhibits reduced sensitivity to proteolysis has at least 85%, at least 88%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions (e.g., at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 20 or more amino acid positions compared to SEQ ID NO: : 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or a sequence having at least 85%, at least 88%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156).

[0131] In some embodiments, the proteolytic sensitivity of the engineered TAL polypeptide will be reduced by at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80% and at least 85% compared to the wild-type *Stanieria cyanosphaera* enzyme of SEQ ID NO:2, and/or at least one reference TAL polypeptide under essentially the same conditions. The proteolytic sensitivity can be measured using any suitable assay system, including, but not limited to the assays described in the Examples.

[0132] In some embodiments, the engineered TAL polypeptide having reduced sensitivity to proteolysis has reduced sensitivity to a composition comprising one or more proteases such as but not limited to pepsin, trypsin, chymotrypsin, carboxypeptidase A and B, peptidases (e.g., amino peptidase, dipeptidase and enteropeptidase) when both the reference TAL and the engineered TAL having the reduced sensitivity are compared and exposed to essentially the same amount and kind of protease under essentially the same conditions.

[0133] In some embodiments, the engineered TAL polypeptide having reduced sensitivity to proteolysis has enzyme activity that is about 1.0 fold, 2-fold, 5-fold, 10-fold, 20-fold, 25-fold, 50-fold,

75-fold, 100-fold, 150-fold, 200-fold or more of the enzymatic activity of the reference TAL. In some embodiments, the engineered polypeptides will have more enzyme activity (as compared to a reference TAL) when activity is measured at a pH range of 4.5 to 7.5; when activity is measured at a pH range of 4.5 to 6.5; when activity is measured at a pH range of 5.0 to 7.5, when activity is measured at a pH range of 5.0 to 6.5; when activity is measured at a pH range of 5.5 to 7.5 and also when activity is measured at a pH range of 5.5 to 6.5. In other embodiments, the engineered TAL polypeptides will have a K_m in the range of 1 μ M to 5mM.

Variants with Increased Tolerance to Acidic pH:

[0134] In some embodiments, the engineered TAL polypeptides of the invention having TAL activity comprise a) an amino acid sequence having at least 85% sequence identity to reference sequence SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or a fragment thereof; b) an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions; and c) which exhibits increased tolerance to acidic pH as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and/or another reference sequence.

[0135] In some embodiments, the engineered TAL that exhibits increased tolerance to acidic pH has at least about 85%, at least about 88%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions (e.g., at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 20 or more amino acid positions compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or a sequence having at least 85%, at least 88%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

[0136] In some embodiments, the engineered TAL polypeptides of the invention having TAL activity comprise a) an amino acid sequence having at least 85% sequence identity to reference sequence SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or a fragment thereof; b) an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions; and c) which exhibits increased tolerance to acidic pH as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and/or another reference sequence.

[0137] In some embodiments, the engineered TAL that exhibits increased tolerance to acidic pH has at least 85%, at least 88%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions (e.g., at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 20 or more amino acid positions compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or a sequence having at least 85%, at least 88%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

[0138] In some embodiments, when all other assay conditions are essentially the same, the engineered TAL polypeptide has increased tolerance to acidic pH as compared to a reference TAL polypeptide. The engineered peptide has an increased tolerance at a pH range between 1.5 to 6.5, and between 1.5 and 5.0, and between 2.0 to 5.5, and between 3.0 and 6.8; between 3.0 and 5.5; between 4.0 and 6.5; between 4.0 and 4.5; between 4.5 and between 5.0; between 4.5 and 5.5, between 4.5 and 6.0; between 4.5 and 6.5; between 5.0 and 6.5; between 5.0 and 6.0; between 5.0 and 5.5; between 5.5 and 6.0; between 6.0 and 6.5 and between 6.5 and 7.0. In some embodiments the increased tolerance to acidic pH will be exhibited at a pH of about 3.5, 4.0, 4.5, 5.0, 5.5, 6.0 and 6.5.

[0139] In some embodiments, the engineered TAL polypeptide having increased tolerance to acidic pH exhibits greater TAL activity as compared to a reference TAL when measured by any standard assay, including, but not limited to the assays described in the Examples.

Variants with Improved Activity:

[0140] In some embodiments, the engineered TAL polypeptides of the invention having TAL activity comprise a) an amino acid sequence having at least 85% sequence identity to reference sequence SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or a fragment thereof; b) an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions; and c) which exhibits improved activity, as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and/or another reference sequence.

[0141] In some embodiments, the engineered TAL that exhibits improved activity has at least about 85%, at least about 88%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and an amino acid residue

difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions (e.g., at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 20 or more amino acid positions compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or a sequence having at least about 85%, at least about 88%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

[0142] In some embodiments, the engineered TAL polypeptides of the invention having TAL activity comprise a) an amino acid sequence having at least 85% sequence identity to reference sequence SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or a fragment thereof; b) an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions; and c) which exhibits improved activity, as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and/or another reference sequence.

[0143] In some embodiments, the engineered TAL that exhibits improved activity has at least 85%, at least 88%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and an amino acid residue difference as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, at one or more amino acid positions (e.g., at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 20 or more amino acid positions compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or a sequence having at least 85%, at least 88%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or greater amino acid sequence identity with SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

[0144] In some embodiments, when all other assay conditions are essentially the same, the engineered TAL polypeptide has improved activity as compared to a reference TAL polypeptide. In some embodiments this activity can be measured under conditions that monitor enzymatic activity at saturating levels of tyrosine, thus assessing the maximum activity of the enzyme (k_{cat}). In other embodiments this activity can be measured under substrate concentrations resulting in one-half, one-fifth, one-tenth or less of maximal activity. Under either method of analysis, the engineered polypeptide has improved activity levels about 1.0 fold, 1.5-fold, 2-fold, 5-fold, 10-fold, 20-fold, 25-fold, 50-fold, 75-fold, 100-fold, or more of the enzymatic activity of the reference TAL. In some embodiments, the engineered TAL polypeptide having improved activity as compared to a reference

TAL when measured by any standard assay, including, but not limited to the assays described in the Examples.

[0145] In light of the guidance provided herein, it is further contemplated that any of the exemplary engineered polypeptides (e.g., SEQ ID NOS: 10-2290; in particular SEQ ID NOS: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156) can be used as the starting amino acid sequence for synthesizing other engineered TAL polypeptides, for example by subsequent rounds of evolution by adding new combinations of various amino acid differences from other polypeptides and other residue positions described herein. Further improvements may be generated by including amino acid differences at residue positions that had been maintained as unchanged throughout earlier rounds of evolution.

Polynucleotides Encoding Engineered Polypeptides, Expression Vectors and Host Cells:

[0146] The present invention provides polynucleotides encoding the engineered TAL polypeptides described herein. In some embodiments, the polynucleotides are operatively linked to one or more heterologous regulatory sequences that control gene expression to create a recombinant polynucleotide capable of expressing the polypeptide. Expression constructs containing a heterologous polynucleotide encoding the engineered TAL polypeptides can be introduced into appropriate host cells to express the corresponding TAL polypeptide.

[0147] As will be apparent to the skilled artisan, availability of a protein sequence and the knowledge of the codons corresponding to the various amino acids provide a description of all the polynucleotides capable of encoding the subject polypeptides. The degeneracy of the genetic code, where the same amino acids are encoded by alternative or synonymous codons, allows an extremely large number of nucleic acids to be made, all of which encode the engineered TAL polypeptide. Thus, having knowledge of a particular amino acid sequence, those skilled in the art could make any number of different nucleic acids by simply modifying the sequence of one or more codons in a way which does not change the amino acid sequence of the protein. In this regard, the present invention specifically contemplates each and every possible variation of polynucleotides that could be made encoding the polypeptides described herein by selecting combinations based on the possible codon choices, and all such variations are to be considered specifically disclosed for any polypeptide described herein, including the variants provided in Table 1-1, 2-1, 3-1, 4-1, 5-1, 6-1, 7-1, 8-1, 9-1, 9-2, 10-1, 10-2, 11-1, 12-1, 13-1, 14-1, 15-1, 16-1, and/or 17-1, as well as SEQ ID NOS: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

[0148] In various embodiments, the codons are preferably selected to fit the host cell in which the protein is being produced. For example, preferred codons used in bacteria are used for expression in bacteria. Consequently, codon optimized polynucleotides encoding the engineered TAL polypeptides contain preferred codons at about 40%, 50%, 60%, 70%, 80%, or greater than 90% of codon positions of the full length coding region.

[0149] In some embodiments, as described above, the polynucleotide encodes an engineered polypeptide having TAL activity with the properties disclosed herein, wherein the polypeptide comprises an amino acid sequence having at least 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more identity to a reference sequence selected from SEQ ID NOS: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or the amino acid sequence of any variant as disclosed in Tables 1-1, 2-1, 3-1, 4-1, 5-1, 6-1, 7-1, 8-1, 9-1, 9-2, 10-1, 10-2, 11-1, 12-1, 13-1, 14-1, 15-1, 16-1, and/or 17-1, and one or more residue differences as compared to the reference polypeptide of SEQ ID NOS: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, or the amino acid sequence of any variant as disclosed in Table 1-1, 2-1, 3-1, 4-1, 5-1, 6-1, 7-1, 8-1, 9-1, 9-2, 10-1, 10-2, 11-1, 12-1, 13-1, 14-1, 15-1, 16-1, and/or 17-1 (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more amino acid residue positions). In some embodiments, the reference sequence is selected from SEQ ID NOS: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

[0150] In some embodiments, the polynucleotide encoding the engineered TAL polypeptides comprises a polynucleotide sequence selected from a polynucleotide sequence encoding the SEQ ID NOS: 3, 13, 85, 333, 387, 603, 735, 789, 1453, 1577, 1659, 1843, 2029, 2113, and/or 2155. In some embodiments, the polynucleotide encoding an engineered TAL polypeptide has at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98%, 99% nucleotide residue identity to SEQ ID NOS: 3, 13, 85, 333, 387, 603, 735, 789, 1453, 1577, 1659, 1843, 2029, 2113, and/or 2155. In some embodiments, the polynucleotides are capable of hybridizing under highly stringent conditions to a reference polynucleotide sequence selected from SEQ ID NOS: 3, 13, 85, 333, 387, 603, 735, 789, 1453, 1577, 1659, 1843, 2029, 2113, and/or 2155, or a complement thereof, or a polynucleotide sequence encoding any of the variant TAL polypeptides provided herein.

[0151] In some embodiments, an isolated polynucleotide encoding any of the engineered TAL polypeptides provided herein is manipulated in a variety of ways to provide for expression of the polypeptide. In some embodiments, the polynucleotides encoding the polypeptides are provided as expression vectors where one or more control sequences is present to regulate the expression of the polynucleotides and/or polypeptides. Manipulation of the isolated polynucleotide prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying polynucleotides and nucleic acid sequences utilizing recombinant DNA methods are well known in the art.

[0152] In some embodiments, the control sequences include among other sequences, promoters, leader sequences, polyadenylation sequences, propeptide sequences, signal peptide sequences, and transcription terminators. As known in the art, suitable promoters can be selected based on the host cells used. For bacterial host cells, suitable promoters for directing transcription of the nucleic acid constructs of the present application, include, but are not limited to the promoters obtained from the *E. coli* lac operon, *Streptomyces coelicolor* agarase gene (dagA), *Bacillus subtilis* levansucrase gene

(*sacB*), *Bacillus licheniformis* alpha-amylase gene (*amyL*), *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), *Bacillus amyloliquefaciens* alpha-amylase gene (*amyQ*), *Bacillus licheniformis* penicillinase gene (*penP*), *Bacillus subtilis* *xylA* and *xylB* genes, and prokaryotic beta-lactamase gene (See e.g., Villa-Kamaroff et al., Proc. Natl Acad. Sci. USA 75: 3727-3731 [1978]), as well as the *tac* promoter (See e.g., DeBoer et al., Proc. Natl Acad. Sci. USA 80: 21-25 [1983]).

Exemplary promoters for filamentous fungal host cells, include promoters obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (*glaA*), *Rhizomucor miehei* lipase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Aspergillus nidulans* acetamidase, and *Fusarium oxysporum* trypsin-like protease (See e.g., WO 96/00787), as well as the NA2-tpi promoter (a hybrid of the promoters from the genes for *Aspergillus niger* neutral alpha-amylase and *Aspergillus oryzae* triose phosphate isomerase), and mutant, truncated, and hybrid promoters thereof. Exemplary yeast cell promoters can be from the genes can be from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* galactokinase (GAL1), *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP), and *Saccharomyces cerevisiae* 3-phosphoglycerate kinase. Other useful promoters for yeast host cells are known in the art (See e.g., Romanos et al., Yeast 8:423-488 [1992]).

[0153] In some embodiments, the control sequence is a suitable transcription terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleic acid sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice finds use in the present invention. For example, exemplary transcription terminators for filamentous fungal host cells can be obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* alpha-glucosidase, and *Fusarium oxysporum* trypsin-like protease. Exemplary terminators for yeast host cells can be obtained from the genes for *Saccharomyces cerevisiae* enolase, *Saccharomyces cerevisiae* cytochrome C (CYC1), and *Saccharomyces cerevisiae* glyceraldehyde-3-phosphate dehydrogenase. Other useful terminators for yeast host cells are known in the art (See e.g., Romanos et al., *supra*).

[0154] In some embodiments, the control sequence is a suitable leader sequence, a non-translated region of an mRNA that is important for translation by the host cell. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used. Exemplary leaders for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase and *Aspergillus nidulans* triose phosphate isomerase. Suitable leaders for yeast host cells include, but are not limited to those obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* 3-

phosphoglycerate kinase, *Saccharomyces cerevisiae* alpha-factor, and *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP).

[0155] The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3' terminus of the nucleic acid sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the present invention. Exemplary polyadenylation sequences for filamentous fungal host cells include, but are not limited to those from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Fusarium oxysporum* trypsin-like protease, and *Aspergillus niger* alpha-glucosidase. Useful polyadenylation sequences for yeast host cells are also known in the art (See e.g., Guo and Sherman, Mol. Cell. Biol., 15:5983-5990 [1995]).

[0156] In some embodiments, the control sequence is a signal peptide coding region that codes for an amino acid sequence linked to the amino terminus of a polypeptide and directs the encoded polypeptide into the cell's secretory pathway. The 5' end of the coding sequence of the nucleic acid sequence may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region that encodes the secreted polypeptide. Alternatively, the 5' end of the coding sequence may contain a signal peptide coding region that is foreign to the coding sequence. Any signal peptide coding region that directs the expressed polypeptide into the secretory pathway of a host cell of choice finds use for expression of the engineered TAL polypeptides provided herein. Effective signal peptide coding regions for bacterial host cells include, but are not limited to the signal peptide coding regions obtained from the genes for *Bacillus* NCIB 11837 maltogenic amylase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus licheniformis* subtilisin, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* neutral proteases (nprT, nprS, nprM), and *Bacillus subtilis* prsA. Further signal peptides are known in the art (See e.g., Simonen and Palva, Microbiol. Rev., 57:109-137 [1993]). Effective signal peptide coding regions for filamentous fungal host cells include, but are not limited to the signal peptide coding regions obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* neutral amylase, *Aspergillus niger* glucoamylase, *Rhizomucor miehei* aspartic proteinase, *Humicola insolens* cellulase, and *Humicola lanuginosa* lipase. Useful signal peptides for yeast host cells include, but are not limited to those from the genes for *Saccharomyces cerevisiae* alpha-factor and *Saccharomyces cerevisiae* invertase.

[0157] In some embodiments, the control sequence is a propeptide coding region that codes for an amino acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is referred to as a "proenzyme," "propeptide," or "zymogen," in some cases). A propeptide can be converted to a mature active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propeptide. The propeptide coding region includes, but is not limited to the genes for *Bacillus subtilis* alkaline protease (aprE), *Bacillus subtilis* neutral protease (nprT), *Saccharomyces cerevisiae* alpha-factor, *Rhizomucor miehei* aspartic proteinase, and *Myceliophthora thermophila*

lactase (See e.g., WO 95/33836). Where both signal peptide and propeptide regions are present at the amino terminus of a polypeptide, the propeptide region is positioned next to the amino terminus of a polypeptide and the signal peptide region is positioned next to the amino terminus of the propeptide region.

[0158] In some embodiments, regulatory sequences are also utilized. These sequences facilitate the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. In prokaryotic host cells, suitable regulatory sequences include, but are not limited to the *lac*, *tac*, and *trp* operator systems. In yeast host cells, suitable regulatory systems include, but are not limited to the ADH2 system or GAL1 system. In filamentous fungi, suitable regulatory sequences include, but are not limited to the TAKA alpha-amylase promoter, *Aspergillus niger* glucoamylase promoter, and *Aspergillus oryzae* glucoamylase promoter.

[0159] In another aspect, the present invention also provides a recombinant expression vector comprising a polynucleotide encoding an engineered TAL polypeptide, and one or more expression regulating regions such as a promoter and a terminator, a replication origin, etc., depending on the type of hosts into which they are to be introduced. In some embodiments, the various nucleic acid and control sequences described above are joined together to produce a recombinant expression vector which includes one or more convenient restriction sites to allow for insertion or substitution of the nucleic acid sequence encoding the variant TAL polypeptide at such sites. Alternatively, the polynucleotide sequence(s) of the present invention are expressed by inserting the polynucleotide sequence or a nucleic acid construct comprising the polynucleotide sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

[0160] The recombinant expression vector may be any vector (e.g., a plasmid or virus), that can be conveniently subjected to recombinant DNA procedures and can result in the expression of the variant TAL polynucleotide sequence. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids.

[0161] In some embodiments, the expression vector is an autonomously replicating vector (i.e., a vector that exists as an extra-chromosomal entity, the replication of which is independent of chromosomal replication, such as a plasmid, an extra-chromosomal element, a minichromosome, or an artificial chromosome). The vector may contain any means for assuring self-replication. In some alternative embodiments, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon may be used.

[0162] In some embodiments, the expression vector preferably contains one or more selectable markers, which permit easy selection of transformed cells. A “selectable marker” is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like. Examples of bacterial selectable markers include, but are not limited to the *dal* genes from *Bacillus subtilis* or *Bacillus licheniformis*, or markers, which confer antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracycline resistance. Suitable markers for yeast host cells include, but are not limited to ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3. Selectable markers for use in a filamentous fungal host cell include, but are not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferases), *bar* (phosphinothricin acetyltransferase), *hph* (hygromycin phosphotransferase), *niaD* (nitrate reductase), *pyrG* (orotidine-5'-phosphate decarboxylase), *sC* (sulfate adenylyltransferase), and *trpC* (anthranilate synthase), as well as equivalents thereof. In another aspect, the present invention provides a host cell comprising a polynucleotide encoding at least one engineered TAL polypeptide of the present application, the polynucleotide being operatively linked to one or more control sequences for expression of the engineered TAL enzyme(s) in the host cell. Host cells for use in expressing the polypeptides encoded by the expression vectors of the present invention are well known in the art and include but are not limited to, bacterial cells, such as *E. coli*, *Vibrio fluvialis*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells (e.g., *Saccharomyces cerevisiae* and *Pichia pastoris* (ATCC Accession No. 201178)); insect cells such as *Drosophila* S2 and *Spodoptera Sf9* cells; animal cells such as CHO, COS, BHK, 293, and Bowes melanoma cells; and plant cells. Exemplary host cells are *Escherichia coli* strains (such as W3110 (Δ fluA) and BL21).

[0163] Accordingly, in another aspect, the present invention provides methods for producing the engineered TAL polypeptides, where the methods comprise culturing a host cell capable of expressing a polynucleotide encoding the engineered TAL polypeptide under conditions suitable for expression of the polypeptide. In some embodiments, the methods further comprise the steps of isolating and/or purifying the TAL polypeptides, as described herein.

[0164] Appropriate culture media and growth conditions for the above-described host cells are well known in the art. Polynucleotides for expression of the TAL polypeptides may be introduced into cells by various methods known in the art. Techniques include, among others, electroporation, biolistic particle bombardment, liposome mediated transfection, calcium chloride transfection, and protoplast fusion.

[0165] The engineered TAL with the properties disclosed herein can be obtained by subjecting the polynucleotide encoding the naturally occurring or engineered TAL polypeptide to mutagenesis and/or directed evolution methods known in the art, and as described herein. An exemplary directed evolution technique is mutagenesis and/or DNA shuffling (See e.g., Stemmer, Proc. Natl. Acad. Sci. USA 91:10747-10751 [1994]; WO 95/22625; WO 97/0078; WO 97/35966; WO 98/27230; WO 00/42651; WO 01/75767 and U.S. Pat. 6,537,746). Other directed evolution procedures that can be

used include, among others, staggered extension process (StEP), in vitro recombination (See e.g., Zhao et al., *Nat. Biotechnol.*, 16:258–261 [1998]), mutagenic PCR (See e.g., Caldwell et al., *PCR Methods Appl.*, 3:S136-S140 [1994]), and cassette mutagenesis (See e.g., Black et al., *Proc. Natl. Acad. Sci. USA* 93:3525-3529 [1996]).

[0166] For example, mutagenesis and directed evolution methods can be readily applied to polynucleotides to generate variant libraries that can be expressed, screened, and assayed.

Mutagenesis and directed evolution methods are well known in the art (See e.g., US Patent Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, 5,837,458, 5,928,905, 6,096,548, 6,117,679, 6,132,970, 6,165,793, 6,180,406, 6,251,674, 6,265,201, 6,277,638, 6,287,861, 6,287,862, 6,291,242, 6,297,053, 6,303,344, 6,309,883, 6,319,713, 6,319,714, 6,323,030, 6,326,204, 6,335,160, 6,335,198, 6,344,356, 6,352,859, 6,355,484, 6,358,740, 6,358,742, 6,365,377, 6,365,408, 6,368,861, 6,372,497, 6,337,186, 6,376,246, 6,379,964, 6,387,702, 6,391,552, 6,391,640, 6,395,547, 6,406,855, 6,406,910, 6,413,745, 6,413,774, 6,420,175, 6,423,542, 6,426,224, 6,436,675, 6,444,468, 6,455,253, 6,479,652, 6,482,647, 6,483,011, 6,484,105, 6,489,146, 6,500,617, 6,500,639, 6,506,602, 6,506,603, 6,518,065, 6,519,065, 6,521,453, 6,528,311, 6,537,746, 6,573,098, 6,576,467, 6,579,678, 6,586,182, 6,602,986, 6,605,430, 6,613,514, 6,653,072, 6,686,515, 6,703,240, 6,716,631, 6,825,001, 6,902,922, 6,917,882, 6,946,296, 6,961,664, 6,995,017, 7,024,312, 7,058,515, 7,105,297, 7,148,054, 7,220,566, 7,288,375, 7,384,387, 7,421,347, 7,430,477, 7,462,469, 7,534,564, 7,620,500, 7,620,502, 7,629,170, 7,702,464, 7,747,391, 7,747,393, 7,751,986, 7,776,598, 7,783,428, 7,795,030, 7,853,410, 7,868,138, 7,783,428, 7,873,477, 7,873,499, 7,904,249, 7,957,912, 7,981,614, 8,014,961, 8,029,988, 8,048,674, 8,058,001, 8,076,138, 8,108,150, 8,170,806, 8,224,580, 8,377,681, 8,383,346, 8,457,903, 8,504,498, 8,589,085, 8,762,066, 8,768,871, 9,593,326, 9,684,771, 9,665,694; and WO 95/22625; WO 97/0078; WO 97/35966; WO 98/27230; WO 00/42651; WO 01/75767; WO 2009/152336, WO 2013/138339, WO 2015/048572, and WO 2015/048573; and all related US and non-US counterparts of these listed patents and applications; Ling et al., *Anal. Biochem.*, 254:157-78 [1997]; Dale et al., *Meth. Mol. Biol.*, 57:369-74 [1996]; Smith, *Ann. Rev. Genet.*, 19:423-462 [1985]; Botstein et al., *Science*, 229:1193-1201 [1985]; Carter, *Biochem. J.*, 237:1-7 [1986]; Kramer et al., *Cell*, 38:879-887 [1984]; Wells et al., *Gene*, 34:315-323 [1985]; Minshull et al., *Curr. Op. Chem. Biol.*, 3:284-290 [1999]; Christians et al., *Nat. Biotechnol.*, 17:259-264 [1999]; Cramer et al., *Nature*, 391:288-291 [1998]; Cramer et al., *Nat. Biotechnol.*, 15:436-438 [1997]; Zhang et al., *Proc. Nat. Acad. Sci. U.S.A.*, 94:4504-4509 [1997]; Cramer et al., *Nat. Biotechnol.*, 14:315-319 [1996]; Stemmer, *Nature*, 370:389-391 [1994]; and Stemmer, *Proc. Nat. Acad. Sci. USA*, 91:10747-10751 [1994]; all of which are incorporated herein by reference).

[0167] In some embodiments, the enzyme clones obtained following mutagenesis treatment are screened by subjecting the enzymes to a defined temperature (or other assay conditions) and measuring the amount of enzyme activity remaining after heat treatments or other assay conditions. Clones containing a polynucleotide encoding a TAL polypeptide are then isolated from the gene,

sequenced to identify the nucleotide sequence changes (if any), and used to express the enzyme in a host cell. Measuring enzyme activity from the expression libraries can be performed using any suitable method known in the art (e.g., standard biochemistry techniques, such as HPLC analysis).

[0168] For engineered polypeptides of known sequence, the polynucleotides encoding the enzyme can be prepared by standard solid-phase methods, according to known synthetic methods. In some embodiments, fragments of up to about 100 bases can be individually synthesized, then joined (e.g., by enzymatic or chemical ligation methods, or polymerase mediated methods) to form any desired continuous sequence. For example, polynucleotides and oligonucleotides disclosed herein can be prepared by chemical synthesis using the classical phosphoramidite method (See e.g., Beaucage et al., *Tetra. Lett.*, 22:1859-69 [1981]; and Matthes et al., *EMBO J.*, 3:801-05 [1984]), as it is typically practiced in automated synthetic methods. According to the phosphoramidite method, oligonucleotides are synthesized (e.g., in an automatic DNA synthesizer), purified, annealed, ligated and cloned in appropriate vectors.

[0169] Accordingly, in some embodiments, a method for preparing the engineered TAL polypeptide can comprise: (a) synthesizing a polynucleotide encoding a polypeptide comprising an amino acid sequence selected from the amino acid sequence of any variant provided in Table 1-1, 2-1, 3-1, 4-1, 5-1, 6-1, 7-1, 8-1, 9-1, 9-2, 10-1, 10-2, 11-1, 12-1, 13-1, 14-1, 15-1, 16-1, and/or 17-1, as well as SEQ ID NOS: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and (b) expressing the TAL polypeptide encoded by the polynucleotide. In some embodiments of the method, the amino acid sequence encoded by the polynucleotide can optionally have one or several (e.g., up to 3, 4, 5, or up to 10) amino acid residue deletions, insertions and/or substitutions. In some embodiments, the amino acid sequence has optionally 1-2, 1-3, 1-4, 1-5, 1-6, 1-7, 1-8, 1-9, 1-10, 1-15, 1-20, 1-21, 1-22, 1-23, 1-24, 1-25, 1-30, 1-35, 1-40, 1-45, or 1-50 amino acid residue deletions, insertions and/or substitutions. In some embodiments, the amino acid sequence has optionally 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 30, 35, 40, 45, or 50 amino acid residue deletions, insertions and/or substitutions. In some embodiments, the amino acid sequence has optionally 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 18, 20, 21, 22, 23, 24, or 25 amino acid residue deletions, insertions and/or substitutions. In some embodiments, the substitutions can be conservative or non-conservative substitutions.

[0170] The expressed engineered TAL polypeptide can be measured for any desired improved property (e.g., activity, selectivity, stability, acid tolerance, protease sensitivity, etc.), using any suitable assay known in the art, including but not limited to the assays and conditions described herein.

[0171] In some embodiments, any of the engineered TAL polypeptides expressed in a host cell are recovered from the cells and/or the culture medium using any one or more of the well-known techniques for protein purification, including, among others, lysozyme treatment, sonication, filtration, salting-out, ultra-centrifugation, and chromatography.

[0172] Chromatographic techniques for isolation of the TAL polypeptides include, among others, reverse phase chromatography high performance liquid chromatography, ion exchange chromatography, hydrophobic interaction chromatography, gel electrophoresis, and affinity chromatography. Conditions for purifying a particular enzyme depends, in part, on factors such as net charge, hydrophobicity, hydrophilicity, molecular weight, molecular shape, etc., and will be apparent to those having skill in the art. In some embodiments, affinity techniques may be used to isolate the improved variant TAL enzymes. In some embodiments utilizing affinity chromatography purification, any antibody which specifically binds the variant TAL polypeptide finds use. For the production of antibodies, various host animals, including but not limited to rabbits, mice, rats, etc., are immunized by injection with a TAL polypeptide (e.g., a TAL variant), or a fragment thereof. In some embodiments, the TAL polypeptide or fragment is attached to a suitable carrier, such as BSA, by means of a side chain functional group or linkers attached to a side chain functional group.

[0173] In some embodiments, the engineered TAL polypeptide is produced in a host cell by a method comprising culturing a host cell (e.g., an *E. coli* strain) comprising a polynucleotide sequence encoding an engineered TAL polypeptide as described herein under conditions conducive to the production of the engineered TAL polypeptide and recovering the engineered TAL polypeptide from the cells and/or culture medium.

[0174] In some preferred embodiments, the invention encompasses a method of producing an engineered TAL polypeptide comprising culturing a recombinant bacterial cell comprising a polynucleotide sequence encoding an engineered TAL polypeptide having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to reference sequences SEQ ID NOS: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and one or more amino acid residue differences as compared to SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156, and/or combinations thereof when aligned, under suitable culture conditions to allow the production of the engineered TAL polypeptide and optionally recovering the engineered TAL polypeptide from the culture and/or cultured bacterial cells.

[0175] In some embodiments, once the engineered TAL polypeptides are recovered from the recombinant host cells or cell culture and they are further purified by any suitable method(s) known in the art. In some additional embodiments, the purified TAL polypeptides are combined with other ingredients and compounds to provide compositions and formulations comprising the engineered TAL polypeptide as appropriate for different applications and uses (e.g., pharmaceutical compositions).

Compositions:

Pharmaceutical Compositions

[0176] The present invention provides engineered TAL polypeptides suitable for use in pharmaceutical and other compositions, such as dietary/nutritional supplements.

[0177] Depending on the mode of administration, the compositions comprising a therapeutically effective amount of an engineered TAL according to the present invention are in the form of a solid, semi-solid, gel, or liquid. In some embodiments, the compositions include other pharmaceutically acceptable components such as diluents, buffers, excipients, salts, emulsifiers, preservatives, stabilizers, fillers, and other ingredients. Details on techniques for formulation and administration are well known in the art and described in the literature.

[0178] In some embodiments, the engineered TAL polypeptides are formulated for use in oral pharmaceutical compositions. Any suitable format for use in delivering the engineered TAL polypeptides find use in the present invention, including but not limited to pills, tablets, gel tabs, capsules, lozenges, dragees, powders, soft gels, sol-gels, gels, emulsions, implants, patches, sprays, ointments, liniments, creams, pastes, jellies, paints, aerosols, chewing gums, demulcents, sticks, suspensions (including but not limited to oil-based suspensions, oil-in water emulsions, etc.), slurries, syrups, controlled release formulations, suppositories, etc. In some embodiments, the engineered TAL polypeptides are provided in a format suitable for injection (i.e., in an injectable formulation). In some embodiments, the engineered TAL polypeptides are provided in biocompatible matrices such as sol-gels, including silica-based (e.g., oxysilane) sol-gels. In some embodiments, the engineered TAL polypeptides are encapsulated. In some alternative embodiments, the engineered TAL polypeptides are encapsulated in nanostructures (e.g., nanotubes, nanotubules, nanocapsules, or microcapsules, microspheres, liposomes, etc.). Indeed, it is not intended that the present invention be limited to any particular delivery formulation and/or means of delivery. It is intended that the engineered TAL polypeptides be administered by any suitable means known in the art, including but not limited to parenteral, oral, topical, transdermal, intranasal, intraocular, intrathecal, via implants, etc.

[0179] In some embodiments, the engineered TAL polypeptides are chemically modified by glycosylation, pegylation (i.e., modified with polyethylene glycol [PEG] or activated PEG, etc.) or other compounds (See e.g., Ikeda, Amino Acids 29:283-287 [2005]; US Pat. Nos. 7,531,341, 7,534,595, 7,560,263, and 7,53,653; US Pat. Appln. Publ. Nos. 2013/0039898, 2012/0177722, etc.). Indeed, it is not intended that the present invention be limited to any particular delivery method and/or mechanism.

[0180] In some additional embodiments, the engineered TAL polypeptides are provided in formulations comprising matrix-stabilized enzyme crystals. In some embodiments, the formulation comprises a cross-linked crystalline engineered TAL enzyme and a polymer with a reactive moiety that adheres to the enzyme crystals. The present invention also provides engineered TAL polypeptides in polymers.

[0181] In some embodiments, compositions comprising the engineered TAL polypeptides of the present invention include one or more commonly used carrier compounds, including but not limited to sugars (e.g., lactose, sucrose, mannitol, and/or sorbitol), starches (e.g., corn, wheat, rice, potato, or

other plant starch), cellulose (e.g., methyl cellulose, hydroxypropylmethyl cellulose, sodium carboxymethylcellulose), gums (e.g., arabic, tragacanth, guar, etc.), and/or proteins (e.g., gelatin, collagen, etc.). Additional components in oral formulations may include coloring and or sweetening agents (e.g., glucose, sucrose, and mannitol) and lubricating agents (e.g., magnesium stearate), as well as enteric coatings (e.g., methacrylate polymers, hydroxyl propyl methyl cellulose phthalate, and/or any other suitable enteric coating known in the art). In some embodiments, disintegrating or solubilizing agents are included (e.g., cross-linked polyvinyl pyrrolidone, agar, alginic acid or salts thereof, such as sodium alginate). In some embodiments, the engineered TAL polypeptide are be combined with various additional components, including but not limited to preservatives, suspending agents, thickening agents, wetting agents, alcohols, fatty acids, and/or emulsifiers, particularly in liquid formulations. In some embodiments, the engineered TAL polypeptides are administered to subjects in combination with other compounds used in the treatment of tyrosinemia and/or alkaptonuria, including but not limited to NTBC, nitisinone, antacids (e.g., omeprazole, esomeprazole and other prazoles), as well as any other suitable compounds. In some additional embodiments, the pharmaceutical composition is suitable for parenteral injection into a human. In yet some additional embodiments, the pharmaceutical composition is coadministered with a phenylalanine ammonia lyase. In some further embodiments, the pharmaceutical composition comprises phenylalanine ammonia lyase. In some embodiments, the pharmaceutical composition comprises a pill, tablet, capsule, or gelcap that further comprises an enteric coating. In yet some additional embodiments, the pharmaceutical composition is coadministered with both nitisinone and a phenylalanine ammonia lyase. In some further embodiments, the pharmaceutical composition comprises both nitisinone and phenylalanine ammonia lyase.

[0182] In some embodiments, the present invention provides engineered TAL polypeptides suitable for use in decreasing the concentration of tyrosine in fluids such as blood, cerebrospinal fluid, etc. The dosages of engineered TAL polypeptide(s) administered to an animal depend upon the condition or disease, the general condition of the animal, and other factors known to those in the art. In some embodiments, the compositions are intended for single or multiple administrations to an animal. In some embodiments, it is contemplated that the concentration of engineered TAL polypeptide(s) in the composition(s) administered to an animal (e.g., a human with tyrosinemia or alkaptonuria) is sufficient to effectively treat, ameliorate and/or prevent the symptoms of disease (e.g., tyrosinemia or alkaptonuria and/or tyrosinemia or alkaptonuria-related conditions, diseases and/or symptoms). In some embodiments, the engineered TAL polypeptides are administered in combination with other pharmaceutical and/or dietary compositions.

Industrial Compositions

[0183] It is contemplated that the engineered TAL polypeptides of the present invention will find use in industrial compositions. In some embodiments, the engineered TAL polypeptides find use in the

production of chemicals (e.g., coumaric acid). In some embodiments, the engineered TAL polypeptides are formulated for use in the food and/or feed industries. In some embodiments, the engineered TAL polypeptides are formulated in granulated or pelleted products which are mixed with animal feed components such as additional enzymes (for example, cellulases, laccases, and amylases).

[0184] In some alternative embodiments, the engineered TAL polypeptides are used in liquid animal feed compositions (e.g., aqueous or oil based slurries). Thus, in some embodiments, the engineered TAL variants of the present invention are sufficiently thermotolerant and thermostable to withstand the treatment used to produce pellets and other processed feed/foods. In some further embodiments, the engineered TAL variants are used to produce tyrosine and/or tyrosine derivatives.

[0185] The engineered TAL polypeptides provided herein also find use in agricultural applications. Indeed, it is contemplated that modulation of TAL activity by using recombinant polypeptides having TAL activity will lead to effective herbicides.

[0186] The foregoing and other aspects of the invention may be better understood in connection with the following non-limiting examples. The examples are provided for illustrative purposes only and are not intended to limit the scope of the present invention in any way.

EXPERIMENTAL

[0187] The following Examples, including experiments and results achieved, are provided for illustrative purposes only and are not to be construed as limiting the present invention.

[0188] In the experimental disclosure below, the following abbreviations apply: ppm (parts per million); M (molar); mM (millimolar), uM and μ M (micromolar); nM (nanomolar); mol (moles); gm and g (gram); mg (milligrams); ug and μ g (micrograms); L and l (liter); ml and mL (milliliter); cm (centimeters); mm (millimeters); um and μ m (micrometers); sec. (seconds); min(s) (minute(s)); h(s) and hr(s) (hour(s)); U (units); MW (molecular weight); rpm (rotations per minute); °C (degrees Centigrade); CDS (coding sequence); DNA (deoxyribonucleic acid); RNA (ribonucleic acid); *E. coli* W3110 (commonly used laboratory *E. coli* strain, available from the Coli Genetic Stock Center [CGSC], New Haven, CT); LB (Luria-Bertani); TB (terrific broth); HPLC (high pressure liquid chromatography); SDS-PAGE (sodium dodecyl sulfate polyacrylamide gel electrophoresis); PES (polyethersulfone); CFSE (carboxyfluorescein succinimidyl ester); IPTG (isopropyl β -D-1-thiogalactopyranoside); PMBS (polymyxin B sulfate); NADPH (nicotinamide adenine dinucleotide phosphate); FIOPC (fold improvements over positive control); PHE and Phe (phenylalanine); TYR and Tyr (tyrosine); PBMC (peripheral blood mononuclear cells); LB (Luria broth); MeOH (methanol); Athens Research (Athens Research Technology, Athens, GA); ProSpec (ProSpec Tany Technogene, East Brunswick, NJ); Sigma-Aldrich (Sigma-Aldrich, St. Louis, MO); Ram Scientific (Ram Scientific, Inc., Yonkers, NY); Pall Corp. (Pall, Corp., Pt. Washington, NY); Millipore (Millipore, Corp., Billerica MA); Difco (Difco Laboratories, BD Diagnostic Systems, Detroit, MI);

Molecular Devices (Molecular Devices, LLC, Sunnyvale, CA); Kuhner (Adolf Kuhner, AG, Basel, Switzerland); Microfluidics (Microfluidics Corp., Westwood, MA); Thermotron (Thermotron, Inc., Holland, MI); Cambridge Isotope Laboratories, (Cambridge Isotope Laboratories, Inc., Tewksbury, MA); Applied Biosystems (Applied Biosystems, part of Life Technologies, Corp., Grand Island, NY); Greiner Bio-One (Greiner Bio-One North America, Monroe, NC); Agilent (Agilent Technologies, Inc., Santa Clara, CA); Thermo Scientific (part of Thermo Fisher Scientific, Waltham, MA); Corning (Corning, Inc., Palo Alto, CA); Megazyme (Megazyme International, Wicklow, Ireland); Enzo (Enzo Life Sciences, Inc., Farmingdale, NY); GE Healthcare (GE Healthcare Bio-Sciences, Piscataway, NJ); Pierce (Pierce Biotechnology (now part of Thermo Fisher Scientific), Rockford, IL); Phenomenex (Phenomenex, Inc., Torrance, CA); Optimal (Optimal Biotech Group, Belmont, CA); and Bio-Rad (Bio-Rad Laboratories, Hercules, CA).

EXAMPLE 1

Synthesis and Assaying of TAL Enzymes with Tyrosine Ammonia Lyase (TAL) Activity

[0189] In this Example, methods used in the synthesis and assaying of TAL enzymes for tyrosine ammonia lyase activity are described.

TAL Gene Acquisition and Construction of Expression Vectors

[0190] Polynucleotide sequences encoding phenylalanine and tyrosine ammonia lyases from *Stanieria cyanosphaera* (SEQ ID NO: 2), *Chroogloeocystis siderophila* (SEQ ID NO: 4), *Flavobacterium johnsoniae* (SEQ ID NO: 6), and *Rhodotorula glutinis* (SEQ ID NO: 8) were synthesized as the genes of SEQ ID NOS: 1, 3, 5, and 7, respectively. These synthetic genes were cloned into a pCK110900 vector system (See e.g., US Pat. No. 7,629,157 and US Pat. Appln. Publ. Nos. 2016/0244787, and 2006/0195947, all of which are incorporated by reference), and subsequently expressed in an *E. coli* strain derived from W3110. In some embodiments, expression vectors lacking antimicrobial resistance markers find use.

High-Throughput (HTP) Growth of Cultures Expressing TAL Enzymes

[0191] Transformed *E. coli* cells were selected by plating onto LB agar plates containing 1% glucose and 30 µg/mL chloramphenicol. After overnight incubation at 37°C, colonies were picked onto NUNC™ (Thermo-Scientific) 96-well shallow flat bottom plates filled with 180 µL/well LB-medium supplemented with 1% glucose and 30 µg/mL chloramphenicol. Cultures were allowed to grow overnight for 18-20 hours in a shaker (200 rpm, 30°C, and 85% relative humidity; Kuhner). Overnight growth samples (20 µL) were transferred into Costar 96-well deep plates filled with 380 µL of TB) supplemented with 30 µg/mL chloramphenicol. Cultures were incubated for 2-3 hours in a shaker (250 rpm, 30°C, and 85% relative humidity; Kuhner) and then induced with 40 µL of 10 mM IPTG in sterile water and incubated overnight for 20-24 hours in a shaker (250 rpm, 30°C, and 85% relative

humidity; Kuhner). Cells were pelleted (4000 rpm x 10 min), supernatants were discarded, and the cells were frozen at -80°C prior to analysis.

Lysis of HTP Cell Pellets

[0192] *E. coli* cell pellets were lysed with 250 µL of lysis buffer (1 mg/ml lysozyme + 0.5 g/L PMBS in 20 mM sodium phosphate pH 8, with 150 mM NaCl). The mixture was agitated for 2 hours at room temperature, and pelleted (4000 rpm x 10 min), after which the clarified lysates were used in HTP assays described herein.

HTP Activity Analysis of Clarified Lysates

[0193] TAL variant activity on tyrosine or phenylalanine was assayed by measuring the formation of coumaric or cinnamic acid, respectively, as determined by the change in absorbance at 290 nm over time. Reactions were prepared by the addition of 160 µL of 2.5 mM tyrosine or phenylalanine dissolved in 200 mM sodium phosphate and 40 µL of clarified lysate to a 96-well UV-STAR® plate (Greiner Bio-One). The reactions were mixed briefly, and the activity was determined by tracking the absorbance at 290 nm over time (every 14-37s over 10 min) using a SPECTRAMAX® Plus 384 or a SPECTRAMAX® 190 (Molecular Devices) absorbance microplate reader. Activity on tyrosine was detected for SEQ ID NOS: 4, 2, 6, and 8 as shown in Table 1-1. Some enzymes also had detectable activity on phenylalanine.

Table 1-1. Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions ¹		
SEQ ID NO: (nt/aa)	2 mM Tyr Activity	2 mM Phe Activity
1/2	++++	
3/4	++	
5/6	+++	
7/8	+	+
¹ Levels of initial activity (milli-Absorbance Units/min) are defined as follows: "+++" >10; "++" > 20; "+++" > 50; and "++++" > 100.		

EXAMPLE 2

Shake Flask Powder (SFP) Production and Characterization Assays for TAL and TAL Variants

[0194] In this Example, methods used for the preparation and characterization of shake flask powders of TAL enzymes with tyrosine ammonia lyase activity are described.

Production of Shake Flask Powders (SFP)

[0195] *E. coli* cultures transformed with plasmids containing TAL variants were plated onto LB agar plates with 1% glucose and in some instances, 30 µg/mL chloramphenicol, and grown overnight at 37°C. A single colony from each culture was transferred to 5 mL of Luria Broth (LB) with 1% glucose and 30 µg/mL chloramphenicol, where appropriate. The cultures were grown for 18 h at 30°C, 250 rpm, and subcultured approximately 1:50 into 250 mL of TB with 30 µg/mL of chloramphenicol. The cultures were grown for approximately 3-4 h at 30°C, 250 rpm, to an OD₆₀₀ of 0.6-0.8, and induced with 1 mM of IPTG. The cultures were grown for 20 h at 30°C, 250 rpm. Cells were harvested by centrifugation (7000 rpm x 10 min, 4°C), and the supernatants were discarded. The pellets were resuspended in 30 mL of 20 mM sodium phosphate, pH 8.0, with 150 mM NaCl in some instances, and lysed using a single pass through a microfluidizer (Microfluidics), at 110 psi. The lysates were pelleted (10,000 x rpm, 30 min, 4°C), and the supernatants were heated for 1-2 hours at 60-65°C in a water bath before being pelleted again (10,000 x rpm, 1 h, 4°C). The resulting supernatants were then frozen and lyophilized to generate powders containing the expressed enzymes.

SFP Characterization Assay for Activity on Tyrosine and Phenylalanine

[0196] Shake flask powders were reconstituted to provide 10-20 g/L powder and were serially diluted to 0.08-10 g/L. Then, 20 µL of these stocks were added to 180 µL of 2.5 mM tyrosine or phenylalanine dissolved in 200 mM sodium phosphate, pH 7.0, in a 96-well UV-STAR® plate (Greiner Bio-One). The reactions were mixed briefly, and the activity was determined by tracking the absorbance at 290 nm over time (every 14-37s over 5 min) using a SPECTRAMAX® Plus 384 or a SPECTRAMAX® 190 (Molecular Devices) absorbance microplate reader. Results for SEQ ID NOS: 2 and 6 are shown in Table 2-1.

[0197] In some cases, TAL enzyme activity on phenylalanine was measured over longer periods of time. Reactions were prepared by adding 20 µL of diluted shake flask powder solution to 180 µL of 2.5 or 12.5 mM phenylalanine dissolved in 200 mM sodium phosphate, pH 7.0. The reactions were mixed briefly, and an initial absorbance was determined by diluting the assay 10-fold in water and measuring the absorbance at 290 nm using a SPECTRAMAX® Plus 384 or a SPECTRAMAX® 190 (Molecular Devices) absorbance microplate reader. After incubation at 37°C for 1-4 h in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm), the final absorbance was measured in a similar manner. Activity was determined by subtracting the initial from the final absorbance.

SFP Characterization Assay for Resistance to Proteases

[0198] To evaluate the relative stability of evolved enzymes to representative proteases, a mix of porcine trypsin (Sigma Aldrich) and bovine chymotrypsin (Sigma Aldrich) were dissolved in 100 mM sodium phosphate, pH 7.0, to a concentration of 8 g/L each and serially diluted 2-fold. Then, 0.5-1

g/L TAL SFP were incubated with 0-4 g/L at 37°C for 1-2 h at 400 rpm in a THERMOTRON® (INFORS) titre-plate shaker. After incubation, 20-40 µL of the protease-treated SFP was added to 160-180 µL of 2.5 mM tyrosine dissolved in 200 mM sodium phosphate, pH 7.0, and enzyme initial activity was measured as described above. Protease resistance was calculated as a percentage of residual activity against the control (i.e., no protease treatment) sample. Results for SEQ ID NOS: 2 and 6 are shown in Table 2-1.

SFP Characterization Assay for pH Tolerance

[0199] To evaluate the relative tolerance of evolved enzymes to acidic pH, SFPs were reconstituted to provide 10 g/L powder and were diluted 10-fold into McIlvaine buffer, pH 4.0-7.0. The mixture was incubated for 1 h at 37°C for 1-1.5 h at 400 rpm in a THERMOTRON® (INFORS) titre-plate shaker. After incubation, the enzyme solutions were briefly centrifuged, and 20 µL of the solutions were added to 180 µL of 2.5 mM tyrosine dissolved in 200 mM sodium phosphate, pH 7.0. Enzymatic activity was determined as described above, and pH tolerance was calculated as a percentage of residual activity against the control (i.e., pH 7.0) sample.

SFP Characterization Assay for Determination of Kinetic Parameters

[0200] To evaluate if the mutations in the TAL variants had altered kinetics, the Michaelis constant (K_m) and maximum velocity (V_{max}) were determined for each variant. To assay, 20 µL of diluted TAL variants at 1 g/L and 180 µL of 2-fold serially diluted tyrosine (0-2.48 mM tyrosine in 200 mM sodium phosphate, pH 7.0), were added to the wells of a 96-well UV-STAR® plate (Greiner Bio-One). The reactions were mixed briefly, and the activity was determined by tracking the absorbance at 290 nm over time (every 14-37s over 5 min) using a SPECTRAMAX® Plus 384 or a SPECTRAMAX® 190 (Molecular Devices) absorbance microplate reader. The V_{max} and K_m for each tested TAL variant was determined by fitting the data to a Michaelis-Menten equation using non-linear regression. Results for SEQ ID NOS: 2 and 6 are shown in Table 2-1.

SFP Characterization Assay for Thermostability

[0201] Improved thermostability is a valuable trait useful in manufacture and storage of enzyme therapeutics and often occurs as a byproduct of other stabilization efforts. To assess the relative stability of the variants produced during the development of the present invention, the thermostability of the variants was assessed as follows: 100 µL of TAL variants at 1 g/L were incubated for 2 h at 60-80°C in a thermocycler. After incubation, samples were briefly centrifuged, and 20 µL of the heat-treated SFP was added to 180 µL of 2.5 mM tyrosine dissolved in 200 mM sodium phosphate, pH 7.0. Enzymatic activity was determined as described above, and thermostability was calculated as a percentage of residual activity against the control (i.e., 60°C) sample. Results for SEQ ID NOS: 2 and 6 are shown in Table 2-1.

Table 2-1. Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions				
SEQ ID NO: (nt/aa)	Tyr Vmax (mAU/min) ¹	Tyr Km (mM) ²	Protease Resistance (% Residual Activity at 0.5 g/L Protease)	Thermostability (% Residual Activity at 60°C)
1/2	+++	+	+	+++
5/6	+	++		++++
¹ Tyr Vmax is defined as follows: "+" = 0.5-1; "++" > 1; and "+++" > 5. ² Tyr Km is defined as follows: "+" = 0.15-0.05; and "++" < 0.05. The % residual activity for protease and thermostability challenges is defined as follows: "+" = 5-50%; "++" > 50%; "+++" > 75%; and "++++" > 90%.				

EXAMPLE 3

TAL Variants of SEQ ID NO: 2

[0202] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 2, for improved tyrosine activity and phenylalanine activity are described. Directed evolution of the TAL encoded by SEQ ID NO: 1, was carried out by constructing libraries of variant genes, using methods known in the art. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates:

[0203] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 1. TAL variant activity on tyrosine and phenylalanine were assayed as described in Example 1, with the following conditions: 20 μ L of HTP lysate diluted 10-fold in water was assayed with 2.2 mM tyrosine for 5 min, 20 μ L of undiluted HTP lysate was assayed with 0.1 mM tyrosine for 10 min, and 50 μ L of undiluted HTP lysate was assayed with 10.5 mM phenylalanine for 10 min. The results of the assays are shown in Table 3-1. Based on these results, SEQ ID NO: 14 was selected for further directed evolution.

Table 3-1 Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 2) ¹			
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 2)	2 mM Tyr FIOPC (Relative to SEQ ID NO: 2)	2 mM Phe FIOPC (Relative to SEQ ID NO: 2)
9/10	N99H/V107A/Y184S	+	+++
11/12	S79T/V107S/P410K	+	++++
13/14	K95A/V107A/Y184S	++	++++
15/16	S79T/P410K	+	+++
17/18	V107S/A401P/A534S	+	+++
19/20	S79T/K95A/V107S	+	++++
21/22	S79T/V107S	+	+++
23/24	K95A/Y184S/A534S	+	+++
25/26	V107A/Y184S/A534S	++	+++
27/28	K95A/V107S/Y184S/A534S	++	+++
¹ All activities were determined relative to the reference polypeptide SEQ ID NO: 2. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; "+++" > 2; and "++++" > 4.			

EXAMPLE 4

TAL Variants of SEQ ID NO: 14

[0204] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 14, for improved tyrosine activity, phenylalanine activity, and protease resistance are described. Directed evolution of the TAL encoded by SEQ ID NO: 13, was carried out by constructing libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

High-Throughput (HTP) Growth of Cultures Expressing TAL Enzymes

[0205] Transformed *E. coli* cells were selected by plating onto LB agar plates containing 1% glucose. After overnight incubation at 37°C, colonies were picked onto NUNC™ (Thermo-Scientific) 96-well shallow flat bottom plates filled with 180 µL/well LB-medium supplemented with 1% glucose. Cultures were allowed to grow overnight for 18-20 hours in a shaker (200 rpm, 30°C, and 85% relative humidity; Kuhner). Overnight growth samples (20 µL) were transferred into Costar 96-well deep plates filled with 380 µL of TB supplemented with 30 µg/mL chloramphenicol. Cultures were incubated for 2-3 hours in a shaker (250 rpm, 30°C, and 85% relative humidity; Kuhner) and then induced with 40 µL of 10 mM IPTG in sterile water and incubated overnight for 20-24 hours in a

shaker (250 rpm, 30°C, and 85% relative humidity; Kuhner). Cells were pelleted (4000 rpm x 10 min), supernatants were discarded, and cells were frozen at -80°C prior to analysis.

Lysis of HTP Cell Pellets

[0206] *E. coli* cell pellets were lysed with 400 µL of lysis buffer (1 mg/ml lysozyme + 0.5 g/L PMBS in 20 mM sodium phosphate pH 8, with 150 mM NaCl). The mixture was agitated for 1.5-2 hours at room temperature, and pelleted (4000 rpm x 10 min) after which the clarified lysates were used in HTP assays or preincubated for 2 h at 65°C in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm). The heat-treated lysates were pelleted (4000 rpm x 10 min), and the supernatants were used in HTP assays.

HTP Activity Analysis of Clarified Lysates

[0207] TAL variant activity was assayed by measuring the formation of coumaric acid as determined by the change in absorbance at 290 nm over time. Reactions were prepared by the addition of 180 µL of 200 mM sodium phosphate, 0.125 or 2.5 mM tyrosine, pH 7.0, and 20 µL of heat-treated clarified lysate (undiluted for 0.125 mM tyrosine or diluted 5-fold for 2.5 mM tyrosine) to a 96-well UV-STAR® plate (Greiner Bio-One). The reactions were mixed briefly, and the activity was determined by tracking the absorbance at 290 nm over time (every 14-37s over 5 min) using a SPECTRA® Plus 384 or a SPECTRAMAX® 190 (Molecular Devices) absorbance microplate reader. The results of these assays are shown in Table 4-1, and SEQ ID NO: 86 was selected for further directed evolution.

[0208] TAL variant activity on phenylalanine was assayed by measuring the formation of cinnamic acid as determined by the change in absorbance at 290 nm over time. Reactions were prepared by adding 160 µL of 200 mM sodium phosphate, 12 mM phenylalanine, pH 7.0, and 40 µL of heat-treated clarified lysate to a 96-well UV-STAR® plate (Greiner Bio-One). The reactions were mixed briefly, and an initial absorbance was determined by measuring the absorbance at 290 nm using a SPECTRAMAX® Plus 384 or a SPECTRAMAX® 190 (Molecular Devices) absorbance microplate reader. After incubation at 37°C for 1.5-3 h in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm), the final absorbance was measured in a similar fashion. Activity was determined by subtracting the initial from the final absorbance, and results are shown in Table 4-1.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease

[0209] TAL variants were challenged with chymotrypsin and trypsin to simulate the environment of the lower intestine. First, 50 µL of protease mix (0.25 mg/mL chymotrypsin (Sigma Aldrich), 0.25 mg/mL trypsin (Sigma Aldrich)) in 100 mM sodium phosphate pH 7.0 and 50 µL of heat-treated clarified lysate were added to a 96-well round bottom plate (Costar). The plates were sealed and incubated for 1 hour at 37°C in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm) prior to analysis. Residual activity was determined by adding 40 µL of the protease-treated lysate to 160 µL of

200 mM sodium phosphate, 2.5 mM tyrosine, pH 7.0, in a 96-well UV-STAR® plate (Greiner Bio-One). The reactions were mixed briefly, and activity was determined as described in Example 3. The results of this assay are shown in Table 4-1.

Table 4-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 14)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 14)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	10 mM Phe FIOPC
29/30	K33D/K34E/Q37S/T90S/K554Q	++	+++	++	++
31/32	A289R/K554Q	++	++	++	++
33/34	K33D/Q66N/A289R/K554Q	++	+++	++	++
35/36	K34E/L46R	+++	+++	++	++
37/38	K33D/Q66N/A289R	++	++	++	++
39/40	K33D/K34E/T90S/A289R/K554Q	++	+++	++	++
41/42	K33D/Q66N	++	++	++	++
43/44	K34E/T90S/A289R/K554Q	++	++	++	++
45/46	K34E/K56G/T90S/A289R	++	++	++	++
47/48	Q66N/T90S/Q279D/A289R/K554Q	++	++	++	++
49/50	T90S/A289R/K554Q	++	++	++	++
51/52	K34E/Q66N/A289R	++	++	++	++
53/54	K33D/K34E/Q37S/L46R/Q279S/K554Q	++	+++	++	++
55/56	K33D/K34E/L46R/Q66N/T90S/A289R	++	++	++	++
57/58	K34E/Q37R/L46R/A289R	++	+++	++	++
59/60	K33D/K34E/Q279S/A289R	++	+++	++	++
61/62	K34E/K56G/T90S	++	++	++	++
63/64	K34E/Q37S/Q66N/Q279S/A289R	++	++	++	++
65/66	Q279S/A289R/K554Q	++	++	++	++
67/68	T90S/A289R/A519P	++	++	++	+
69/70	K34E/T90S/A519P	++	++	++	++
71/72	Q66N/T90S/A289R/K554Q	++	++	++	++
73/74	A289R/A519P/K554Q	++	++	++	++
75/76	L46R/Q66N/A289R/A519P/K554Q	++	++	++	++
77/78	S79T/E304G/L361M	++	+++	++	+
79/80	S79T/Q111K/N531D	++	+++	++	++
81/82	S79T/S407V/L461M	++	+++	+	++
83/84	S79T/Q111K/Y234H/L361M/C500T	++	++++	+	++

**Table 4-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine
Under Various Conditions (Relative to SEQ ID NO: 14)¹**

SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 14)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	10 mM Phe FIOPC
85/86	S70K/S79T/Y234H/L361M/S407V	++	++++	+	++
87/88	E304G/L361M	++	+++	++	+
89/90	S79T/E304G/L461M/N531D	++	+++	++	+
91/92	S70K/E304G/S407V/L461M	++	+++	++	++
93/94	S79T/Q111K/Y234H/N531D	++	+++	++	++
95/96	A36V/S407V/L461M/C500T/N531D	++	++	++	++
97/98	A36V/Q111K/E304G/L461M/N531D	++	++	++	+
99/100	L461M/C500T	++	++	++	++
101/102	S70K/Q111K/L461M/C500T/N531D	++	+++	++	++
103/104	L361M/C500Q/N531D	++	++	++	+
105/106	A36V/S79T/S407V/L461M/C500T/N531D	++	++++	++	++
107/108	A36V/S70K/Y234H/R302M/L461M/C500T	++	+++	++	
109/110	A36V/S79T	+	+++	+	++
111/112	A36V/S79T/E304G/S407V	+	+++	++	+
113/114	N531D	++	++	++	++
115/116	S79T/Q111K/L361M	++	++++	++	++
117/118	S548R	++	+++	++	++
119/120	A544E	++	+++	++	++
121/122	K28G	+++	+++	+++	++
123/124	E522K	++	++++	++	++
125/126	A540R	++	+++	++	++
127/128	A544G	++	+++	++	++
129/130	T547S	++	+++	++	++
131/132	Q558A	++	++	++	++
133/134	A544S	++	+++	+++	++
135/136	R524Y	++	++	++	++
137/138	L295Q	+++	++	+++	+
139/140	T547C	++	++	++	++
141/142	L541A	++	+++	++	++
143/144	I491V	++	++	++	++
145/146	E522G	++	+++	++	++
147/148	Q66S	++	++	++	++
149/150	S548Q	++	++	++	++

Table 4-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine
Under Various Conditions (Relative to SEQ ID NO: 14)¹

SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 14)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	10 mM Phe FIOPC
151/152	K518E	++	+++	++	++
153/154	P29E	++	+++	++	++
155/156	E522R	++	++++	++	++
157/158	T547Q	+++	+++	++	++
159/160	S548T	++	+++	++	++
161/162	K490I	+++	++	+++	++
163/164	K518V	+++	+++	++	++
165/166	V88Q	+++	++	+++	++
167/168	E522V	++	+++	++	++
169/170	K201R	++	++	++	++
171/172	K554S	++	+++	++	++
173/174	K28N	++	+++	++	++
175/176	K28C	++	+++	++	++
177/178	A278S	++	++	++	++
179/180	I491L	++	++	++	++
181/182	K33N	++	+++	++	++
183/184	P29R	++	++	++	++
185/186	A540E	++	+++	++	++
187/188	R524Q	+++	+++	+++	++
189/190	T547A	+++	+++	++	++
191/192	H131M	+++	++	+++	++
193/194	S548K	++	+++	++	++
195/196	E522Y	++	++	++	++
197/198	P29A	++	++	++	++
199/200	K554Y	++	++	++	+
201/202	V560R	++	++	++	++
203/204	K490A	+++	++	+++	++
205/206	T49N	++	+++	++	++
207/208	K28A	++	++	++	++
209/210	T547K	++	+++	++	++
211/212	A519Q	++	+++	+++	++
213/214	L46R	++	++	++	++
215/216	R524A	++	++	++	++
217/218	Q558H	++	++	++	++
219/220	R524T	++	++	++	++
221/222	Q66R	+++	+++	+++	++
223/224	V88E	+++	++	++	+
225/226	Q37A	++	++	++	++

Table 4-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine
Under Various Conditions (Relative to SEQ ID NO: 14)¹

SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 14)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	10 mM Phe FIOPC
227/228	S548A	++	++	++	++
229/230	V560T	++	++	++	++
231/232	P272S	++	++	++	++
233/234	A519L	++	++	++	++
235/236	K490V	++	++	++	++
237/238	K554R	++	+++	++	++
239/240	L510K	++	+++	++	++
241/242	T547G	++	++	++	++
243/244	S548G	++	+++	++	++
245/246	R524L	+++	+++	+++	++
247/248	Q558S	+++	+++	++	++
249/250	T547R	+++	+++	+++	++
251/252	N557E	+++	+++	+++	+++
253/254	T49D	+++	+++	+++	+++
255/256	E72T	+++	++	++	+
257/258	Q558D	+++	+++	+++	+++
259/260	V560G	++	++	++	++
261/262	E523D	++	+++	++	++
263/264	P29G	++	++	++	+++
265/266	E523I	+	+	+	+
267/268	A519E	+++	+++	++	++
269/270	E523S	++	++	++	++
271/272	K554E	++	+++	++	++
273/274	L46T	++	++	++	++
275/276	R524I	+++	++	++	++
277/278	Q305H	+++	++	+++	++
279/280	V560M	++	+++	++	++
281/282	Q142R	++	++	++	++
283/284	A519D	++	++	++	++
285/286	E523A	++	++	++	++
287/288	E523H	++	++	++	++
289/290	H131S	++	++	++	++
291/292	K28T	++	++	++	++
293/294	H131W	++	++	++	++
295/296	A69S	++	++	++	++
297/298	K490S	++	+	++	++
299/300	P29W	++	++	++	++
301/302	A519P	++	++	++	++

**Table 4-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine
Under Various Conditions (Relative to SEQ ID NO: 14)¹**

SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 14)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	10 mM Phe FIOPC
303/304	Q37D	+++	+++	+++	+++
305/306	H131G	+	+++	++	++++
307/308	A350G	+++	+++	++	++
309/310	K56R	++	++	++	++
311/312	E198R	+	+	++	+
313/314	S521D	+++	+++	++	++
315/316	Q499T	++	++	++	++
317/318	K56G	+++	+++	+++	+++
319/320	N557R	++	++	++	++
321/322	A544R	+++	+++	++	++

¹All activities were determined relative to the reference polypeptide SEQ ID NO: 14. Levels of increased activity are defined as follows: "+" = 0.9 to 1.1; "++" > 1.1; "+++" > 2; and "++++" > 3.

EXAMPLE 5

TAL Variants of SEQ ID NO: 86

[0210] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 86 for improved tyrosine activity, phenylalanine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 85, was carried out by constructing libraries of variant genes using methods known in the art. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0211] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine and phenylalanine were assayed as described in Example 4, with the following conditions: 20 μ L of HTP lysate diluted 4- or 5-fold in water was assayed with 2.2 mM tyrosine for 5 min, 20 μ L of undiluted HTP lysate was assayed with 0.1 mM tyrosine for 5 min, and 20 μ L of undiluted HTP lysate was assayed with 10.8 mM phenylalanine for 2 h. The results of the assays are shown in Table 5-1. SEQ ID NO: 334 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease

[0212] TAL variants were challenged with chymotrypsin and trypsin, and 50 μ L of heat-treated clarified lysate were incubated with 50 μ L of protease mix consisting of 8 mg/mL chymotrypsin (Sigma Aldrich) and 8 mg/mL trypsin (Sigma Aldrich) in 100 mM sodium phosphate pH 7.0.

Residual activity on tyrosine was measured as described in Example 4, and the results of this assay are shown in Table 5-1.

HTP Activity Analysis of Clarified Lysates Pretreated with Acidic Buffer

[0213] TAL variants were challenged with acidic buffer to simulate the gastric environment. First, 50 μ L of McIlvaine buffer pH 4 or 4.2, and 50 μ L of heat-treated clarified lysate were added to a 96-well round bottom plate (Costar). The plates were sealed and incubated for 1 hour at 37°C in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm) prior to analysis. After incubation, the lysate solutions were briefly centrifuged, and residual activity was determined by adding 40 μ L of the acidic buffer-treated lysate to 160 μ L of 200 mM sodium phosphate, 2.5 mM tyrosine, pH 7.0, in a 96-well UV-STAR® plate (Greiner Bio-One). The reactions were mixed briefly, and activity was determined as described in Example 4. The results of this assay are shown in Table 5-1.

Table 5-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 86) ¹						
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 86)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC	10 mM Phe FIOPC
323/324	K33D/K34E/Q66N/A289R/E522K/N531D	++	++	++	++++	++
325/326	K33D/K34E/K70S/H234Y/A289R/A519P	++	++	++	++++	++
327/328	K34E/Q66N/K70S/H234Y/K518V/A519P/T547Q	+++	+++	++	++++	++
329/330	K33N/K34E/T49N/H234Y/N531D/T547Q/K554Q	++	++	++	++++	++
331/332	K34E/Q66N/N531D/K554Q	+++	+++	++	+++	++
333/334	K34E/A289R/E522K/A544E/K554Q	+++	++	+++	++++	++
335/336	K33D/K34E/K70S/H234Y/K518V/A519P/T547Q/K554Q	++	++	++	+++	++
337/338	Q66N/K70S/H234Y	++	++	+	+++	+
339/340	K34E/H234Y/E522K/K554Q	++	++	+++	++++	++
341/342	K34E/K70S/A289R/E522K	++	++	++	++	+
343/344	K34E/A289R	++	++	++	+++	++
345/346	H234Y/N531D/A544E/T547Q	++	++	++	+++	++

Table 5-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 86)¹						
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 86)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC	10 mM Phe FIOPC
347/348	K33D/K34E/Q66N/K70S/A519P/N531D	+++	+++	+	+++	++
349/350	K34E/T49N/Q66N/N531D	+++	++	++	+++	++
351/352	K34E/K70S/H234Y/A289R/E522K	++	++	++	++++	+
353/354	K28N/K34E/T49N/K70S/H234Y/A289R/A544E/K554Q	+++	++	++	+++	++
355/356	K33D/K34E/K70S/A289R/E522K/K554Q	+++	++	++	+++	++
357/358	K33D/K34E/A289R/E522K/N531D	+++	++	++	++++	++
359/360	K34E/K70S/H234Y/K554Q	+++	++	++	++++	++
361/362	K34E/T49N/A289R/A544E/T547Q	+++	++	+++	+++	++
363/364	K34E/A289R/E522K/N531D	+++	+++	++	++++	++
365/366	K34E/Q66N/K554Q	+++	++	+++	+++	++
367/368	K34E/A544E	++	++	+++	+++	++
369/370	K34E/T49N/H234Y/N531D/K554Q	+++	+++	+++	++++	++
371/372	K34E/E522K	++	++	+++	+++	++
¹ All activities were determined relative to the reference polypeptide SEQ ID NO: 86. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; "+++" > 2; and "++++" > 3.						

EXAMPLE 6

TAL Variants of SEQ ID NO: 334

[0214] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 334 for improved tyrosine activity, phenylalanine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 333, was carried out by constructing libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0215] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4, with the following conditions: 20 μ L of HTP lysate diluted 4-10-fold in water was assayed with 2.2 mM tyrosine for 5 min and 20 μ L of undiluted HTP lysate was assayed with 0.1 mM tyrosine for 5 min. TAL variant activity on phenylalanine was assayed as described in Examples 1 and 4, with the following conditions: 20 μ L of undiluted HTP lysate was assayed with 2.2 mM phenylalanine for 5 min at room temperature or for 1-3 h at 37°C. The results of the assays are shown in Table 6-1. SEQ ID NO: 388 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease

[0216] TAL variants were challenged with chymotrypsin and trypsin as described in Example 4, and 50 μ L of heat-treated clarified lysate was incubated with either 50 μ L 8 g/L protease mix for 1 h at 37°C or with 4 g/L protease mix for 2 h at 37°C. Residual activity was determined by adding 20 μ L of the protease-treated lysate to 180 μ L of 200 mM sodium phosphate, 2.5 mM tyrosine, pH 7.0, in a 96-well UV-Star® plate (Greiner Bio-One). The reactions were mixed briefly, and activity was determined as described in Example 4. The results of this assay are shown in Table 6-1.

HTP Activity Analysis of Clarified Lysates Pretreated with Acidic Buffer

[0217] TAL variants were challenged with acidic buffer as described in Example 5, and 50 μ L of heat-treated clarified lysate was incubated with 50 μ L McIlvaine buffer pH 4. Residual activity was determined as described in Example 5, and the results of this assay are shown in Table 6-1.

Table 6-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 334) ¹						
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 334)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC	2 mM Phe FIOPC
373/374	I336V	++	++	+	++	+
375/376	L506R	++	+	+	+	+
377/378	A43T/S59A/L93Q/L506R	+	+	+	+	+
379/380	Q237R/N238V/L506R	+	+	+	+	+
381/382	A65N/I336V	++	+	+	+	+
383/384	P306L/L506R	++	+	+	++	+
385/386	A43T/P306L	++		+	++	+

Table 6-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 334)¹						
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 334)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC	2 mM Phe FIOPC
387/388	L93Q/L506R	+	++	+	+	+
389/390	P306L	++	+	+	++	+
391/392	A43T/P306L/L506R	+		+	+	+
393/394	R103W/P306L/L506R	+	+	+	++	+
395/396	K56G/H234Y/C500T	+	++	+	++	+
397/398	Q37D/T49N/K56G/C500T/R524Q	++	++	+	+	+
399/400	Q66N	++	++	++	++	+
401/402	Q37D/T49N/Q111K/R524Q	++	+	++	++	+
403/404	Q66N/Q111K/H234Y/C500T	+	++	+	+	+
405/406	T49N/K56G/Q66N/Q111K/T153N/H234Y/C500T/R524Q	+	+	+	++	+
407/408	Q37D/Q111K	++	++	+	+	+
409/410	H234Y	++		++	++	+
411/412	Q37D/H234Y	+	+	+	++	+
413/414	Q37D/T49N/Q66N/Q111K/H234Y	+	++	+	+	+
415/416	Q111K/M361L	++		+	++	+
417/418	Q558D	+	++	+	++	+
419/420	T49N/Q66N	++	+	+	++	+
421/422	Q37D/T49N/K56G/Q66N/Q111K	+	+	+	++	+
423/424	M361L/R524Q/N557E/Q558D	+	+	+	+	+
425/426	Q37D/T49N/K56G/H234Y/N557E	++	+	+	++	+
427/428	Q37D/Q111K/M361L/C500T/N557E/Q558D	++	++	++	++	+
429/430	Q111K/H234Y/S548K/Q558D	++	++	++	+	+
431/432	H234Y/R524Q	++	++	++	+	+

Table 6-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 334)¹						
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 334)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC	2 mM Phe FIOPC
433/434	K56G/Q111K/H234Y	++	+	++	++	+
435/436	T421S	++		++	+	+
437/438	A107T/G417A/T421A	+				+
439/440	G417A/T421S	++	++	+	+	++
441/442	A107T	++	+	++	++	+
443/444	R103W/T421S		+	+	+	++
445/446	A172S					+
447/448	R103W/A107T/G417A/T421S	+	+	+	++	+
449/450	R103W		+	+	+	+
451/452	Y104F/H105M					++++
453/454	A504R	+	+	+	+	+
455/456	S328A	+	+	+	+	+
457/458	E145V	+	+	+	+	+
459/460	Q471Y	+	+	+		+
461/462	R103L	+	+	+	+	++
463/464	G549D	+	+	+	+	+
465/466	C61V		++	+		+
467/468	E304N		++			+
469/470	V407T	+		+	+	+
471/472	L211K	+				+
473/474	H155S	+	+	+	+	+
475/476	T146K	+	+	++	+	+
477/478	A95K	+	+	+	+	
479/480	A65M			+		+
481/482	A286Q	+	+	+	+	+
483/484	A95V	+		++	+	+
485/486	T31S	+	+	+		+
487/488	P197T	+		+		+
489/490	V407K	+	+	+		+

Table 6-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 334)¹

SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 334)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC	2 mM Phe FIOPC
491/492	H155L	+	+	+		+
493/494	A286R	+		+		+
495/496	L506V	+	+	++	+	+

¹All activities were determined relative to reference polypeptide SEQ ID NO: 334. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; "+++" > 2; and "++++" > 3.

EXAMPLE 7

TAL Variants of SEQ ID NO: 388

[0218] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 388 for improved tyrosine activity, phenylalanine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 387, was carried out by constructing libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0219] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4, with the following conditions: 20 μ L of HTP lysate diluted 10-fold in water was assayed with 2.2 mM tyrosine for 5 min and 20 μ L of undiluted HTP lysate was assayed with 0.1 mM tyrosine for 5 min. TAL variant activity on phenylalanine was assayed as described in Example 4 with the following conditions: 20 μ L of undiluted HTP lysate was assayed with 2.2 mM phenylalanine for 5 min at room temperature or for 2 h at 37°C. The results of the assays are shown in Table 7-1. SEQ ID NO: 604 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease

[0220] TAL variants were challenged with chymotrypsin and trypsin as described in Example 4, and 50 μ L of heat-treated clarified lysate was incubated with 50 μ L 8 g/L protease mix for 2 h at 37°C. Residual activity was determined as described in Example 6. The results of this assay are shown in Table 7-1.

HTP Activity Analysis of Clarified Lysates Pretreated with Acidic Buffer

[0221] TAL variants were challenged with acidic buffer as described in Example 5, and 50 μ L of heat-treated clarified lysate was incubated with 50 μ L McIlvaine buffer pH 4. Residual activity was determined by adding 20 μ L of the acidic buffer-treated lysate to 180 μ L of 200 mM sodium phosphate, 2.5 mM tyrosine, pH 7.0, in a 96-well UV-Star[®] plate (Greiner Bio-One). The reactions were mixed briefly, and activity was determined as described in Example 4. The results of this assay are shown in Table 7-1.

Table 7-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 388)¹						
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to ID NO: 388)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC	2 mM Phe FIOPC
497/498	Q66N/R103L/E145V/H234Y/T421S	++	++	++	++++	++
499/500	S59A/E145V	++	++	++	++++	++
501/502	T49N/S59A/Q66N/Q111K/E145V/H234Y	++	+++	++	++++	+
503/504	Q111K/E145V/H234Y	++	++	++	++++	+
505/506	K56G/Q66N/E145V/C500T	++	++	++	++++	+
507/508	K56G/S59A/Q66N/H234Y	++	+++	++	++++	++
509/510	R103L/Q111K/E145V/H234Y/T421S	++	++	++	++++	++
511/512	Q111K/H234Y	++	++	++	++++	++
513/514	K56G/S59A/Q111K/E145V/H234Y/T421S	++	++	++	++++	++
515/516	T49N/K56G/S59A/H234Y/C500T	++	+++	++	++++	++
517/518	S59A/H234Y	++	++	++	++++	++
519/520	E145V/H234Y/C500T	++	++	++	++++	+
521/522	K56G/R103L/Q111K/E145V/H234Y/C500T	++	+++	++	++++	++
523/524	Q37D/R103L/Q111K/E145V/T421S/C500T/R524Q	++	++	++	++++	++
525/526	K56G/S59A/Q111K/E145V	++	++	++	++++	+

Table 7-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 388) ¹						
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to ID NO: 388)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC	2 mM Phe FIOPC
527/528	S59A/R103L/E145V/H234Y/ T421S/C500T	++	++	++	++++	++
529/530	T49N/S59A/E145V/H234Y/T 421S	++	++	++	++++	++
531/532	Q37D/T49N/K56G/S59A/E14 5V	++	+++	++	++	++
533/534	S59A/R103L/H234Y/T421S	++	++	++	++++	++
535/536	C61V/V407T	+	++	+		++
537/538	A286Q/S328A/V407T/A504R /G549D	++	++	++	++++	+
539/540	C61V/S328A/A504R	+	++	+	++++	++
541/542	A95K/V407T	++	++	++		+
543/544	T31S/A95K/A286Q/A504R/G 549D	++	++	+	++++	+
545/546	C61V/A95K/S328A/V407T	++	+++	++	++	+
547/548	T31S/A95K/S328A/A504R	++	++	++	+	+
549/550	C61V/A95K/V407T	++	+++	++	++	++
551/552	G549D	++	++	+	++++	++
553/554	A95K/A286Q	++	++	++		+
555/556	C61V/A504R	+	++	+	++++	++
557/558	A95K/A286Q/S328A/A504R	++	++	++	++++	+
559/560	A95K/H155S/A286Q/G549D	++	++	++	++++	+
561/562	T31S/A95K/H155S/A286Q/A 504R/G549D	++	++	++	++++	+
563/564	T31S/A95K/G549D	++	++	++	++++	+
565/566	C61V/A95K/A504R/T547Q	++	+++	++	+++	++
567/568	A95K/H155S/A286Q/S328A/ V407T/A504R	++	++	++	+++	+
569/570	T31S/A95K/A504R	++	++	++	++	+
571/572	A95K/A286Q/T547Q	++	++	++		+

Table 7-1. Relative Activity of TAL Variants on Tyrosine and Phenylalanine Under Various Conditions (Relative to SEQ ID NO: 388)¹						
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to ID NO: 388)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC	2 mM Phe FIOPC
573/574	C61V/S328A/A504R/G549D	+	+++	+	++++	++
575/576	T31S/C61V/A95K/Q471Y/A504R	++	+++	++	++++	++
577/578	C61V/A286Q/V407T	+	+++	++	++	++
579/580	A95K/S328A/A504R	++	++	++	++	+
581/582	A95K/V407T/A504R	++	++	++	++	+
583/584	T31S/C61V/V407T/A504R	+	++	+	++	++
585/586	A95K/G549D	++	+++	++	++++	+
587/588	T31S/A95K/A286Q/A504R	++	++	++	++	+
589/590	T31S/A95K/Q237K/A504R/T547Q/G549D	++	+++	++	++++	+
591/592	C61V	+	+++	+	++	++
593/594	C61V/A95K/S328A/G549D	++	+++	++	++++	++
595/596	C61V/A95K/A286Q	++	+++	++	+	++
597/598	C61V/A95K/A286Q/S328A/A504R	++	+++	++	++++	++
599/600	C61V/A95K/H155S/A286Q/V407T/Q471Y	++	++	++	++++	+
601/602	T31S/C61V/A95K/V407T/A504R	++	++	++	++	++
603/604	A95K/A286Q/S328A/V407T/A504R	++	++	++	+++	+
605/606	A95K/G287S/A504R/G549D	++	++	++	++++	+
607/608	T31S/C61V/A95K/A286Q/S328A	++	+++	++	+	++
609/610	C61V/S328A	+	++	+	++	++
611/612	A95K/A504R/T547Q	++	++	++	+	+
613/614	C61V/A95K/H155S/V407T	++	++	+	++++	+
¹ All activities were determined relative to reference polypeptide SEQ ID NO: 388. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; "+++" > 2; and "++++" > 3.						

EXAMPLE 8**TAL Variants of SEQ ID NO: 604**

[0222] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 604, for improved tyrosine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 603, was carried out by constructing libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0223] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4, with the following conditions: 20 μ L of HTP lysate diluted 10-fold in water was assayed with 2.2 mM tyrosine for 5 min and 20 μ L of undiluted HTP lysate was assayed with 0.1 mM tyrosine for 5 min. The results of the assays are shown in Table 8-1. SEQ ID NO: 736 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease

[0224] TAL variants were challenged with chymotrypsin and trypsin as described in Example 4, and 50 μ L of HTP lysate diluted 2-fold was incubated with 50 μ L 3 g/L protease mix for 1 h at 37°C. Residual activity was determined as described in Example 4. The results of this assay are shown in Table 8-1.

HTP Activity Analysis of Clarified Lysates Pretreated with Acidic Buffer

[0225] TAL variants were challenged with acidic buffer as described in Example 5, and 40 μ L of heat-treated clarified lysate was incubated with 60 μ L McIlvaine buffer pH 4. Residual activity was determined as described in Example 5. The results of this assay are shown in Table 8-1.

Table 8-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 604)					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 604)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
615/616	N531D	++	+	++	++
617/618	Q37A/K56G/S59A/H234Y/N5 31D	++	++	++	++++
619/620	A36V/H131M	+	+	++	++++

Table 8-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 604)					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 604)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
621/622	Q37A/K56G/S59A/R103L/E145V/H234Y/A328Q/Q471Y/N531D	++	++	++	++++
623/624	A36V/Q37A/H131M/E145V/H234Y/A328S	+	+	+	++++
625/626	A36V/Q37A/E145V/H234Y	+	++	++	++++
627/628	K56G/S59A/R103L/Q471Y/N531D	+	+	++	+++
629/630	A36V/S59A/H234Y/A328S		+	+	++++
631/632	Q37A/H234Y/Q471Y	+	++	++	++++
633/634	A36V/K56G/E145V/H234Y/A328S	+	++	++	++++
635/636	H234Y/N531D	++	+	++	++++
637/638	A36V/Q37A/R103L/H234Y	+	++	+	++++
639/640	H234Y/A328Q	++	++	++	++++
641/642	H234Y/A328S/Q471Y	+	++	++	++++
643/644	Q37A/K56G/H234Y/N531D	+	+	+	++++
645/646	A36V/R103L/E145V/A328S/N531D	+	++	++	++++
647/648	A36V/Q37A/S59A/H131M/N531D	++	+	++	++++
649/650	A36V/S59A/N531D	+	++	++	++++
651/652	K56G/S59A/Q471Y/N531D	++	++	++	+++
653/654	Q37A/K56G/S59A/H234Y/A328S/R524L/N531D			+	++++
655/656	H234Y			+	++++
657/658	S59A/A328Q/R524L/N531D	++	+	++	++++
659/660	A36V/H234Y/N531D	+	+	++	++++
661/662	A36V/Q37A/K56G/S59A/E145V/H234Y/A328S	+	++	+	++++
663/664	Q37A/S59A/H234Y	+	+	+	++++

Table 8-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 604)					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 604)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
665/666	A36V/Q37A/H234Y/A328Q/N531D	+	+	++	++++
667/668	H131M/H234Y/A328Q	+++		++	++++
669/670	A36V/Q37A/E145V/H234Y/A328S/Q471Y/N531D	+	+	++	++++
671/672	K518V/A519E/S548K/G549D	++	++	++	++++
673/674	L46T/T49D/A519E	+++	++	++	++
675/676	L46R/H155L	++	++	++	+
677/678	K33N/L46T/K518V/A534S/S548K/G549D	++	++	++	++++
679/680	I336V/A519P	++	++	++	+++
681/682	T49D/A519P	+++	+++	++	++
683/684	K33N/L46T/T49D/G549D	++	++	+	++++
685/686	S548K/G549D	+	+	++	++++
687/688	L46T/S548K	+++	++	++	+++
689/690	G549D	++	++	++	++++
691/692	K33N/T49D/I336V	+++	+++	++	+++
693/694	K33N/L46T/T49D/I336V/A519E/S548K/G549D	++	++	+	++++
695/696	K33N/L46T/T49D	+++	+++	++	++
697/698	A519P	++	+	++	++
699/700	L46R/T49D/A519P	+++	+++	++	+++
701/702	K33N/L46R/T49D/G549D	+++	+++	++	++++
703/704	K33N/I336V/A519P	++	++	++	+++
705/706	L46R/T49D/K518V/A519E/S548K/G549D	++	++	++	++++
707/708	L46R/T49D	++	++	++	++
709/710	K33N/L46T/A519E	++	+	++	++
711/712	L541A			+	+
713/714	S521D	++	++	++	++
715/716	Q66R/A540R	++	+	++	+++

Table 8-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 604)					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 604)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
717/718	E523D	+		+	+
719/720	P29E/Q66N/Q111K/A540R	++	++	++	+
721/722	Q111K	++	++	++	+++
723/724	Q111K/E523A/N557E	++	++	++	++
725/726	P29E/Q111K	+	+	+	
727/728	P29G/Q66N/Q111K	+	+	+	
729/730	P29E/Q111K/E523D	+	+	+	
731/732	Q111K/L510K/S521D/E523A/ L541A/Q558D	++	+	++	+++
733/734	F14S/S114P/E283D/R289Q	++	++	++	++++
735/736	F14S/K56R/S114P	++	++	++	++++
737/738	K56R/S114P/I291V	++	++	++	++++
739/740	F14S/S114P/K518Q	++	++	++	++++
741/742	K56R/S114P/E206P/E283D	++	++	++	++++
743/744	F14S/E283D/R289Q/I562S	++	++	++	+
745/746	S114P/E283D/I291V	++	++	++	++++
747/748	K56R/S114P/I291V/K518Q/I5 62S	++	+	++	++++
749/750	S114P/I562S	++	++	++	++++
751/752	K56R/S114P/K518Q	+++	++	++	++++
753/754	F14S/S114P/E283S/R289Q/I56 2S	++	++	++	++++
755/756	S114P/E283D/R289Q/Q305E/ K518Q	+++	++	++	++++
757/758	S114P/R289Q/I562S	++	++	++	++++
759/760	S114P/K518Q/I562S	++	++	++	++++
761/762	F14S/S114P/E283D/R289Q/I29 1V	++	++	++	++++
763/764	S114P/I291V/K518Q	++	++	++	++++
765/766	F14S/H234L/E283D/I291V/Q3 05E	++	++	++	++++
767/768	K56R/K518Q	++	++	++	+

Table 8-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 604)					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 604)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
769/770	S114P/E283D/R289Q/I291V	++	++	++	++++
771/772	S114P/I291V	++	+	++	++++
773/774	S114P/R289Q	++	++	++	++++
775/776	S114P	++	++	++	++++
777/778	F14S/S114P/I291V/K518Q/I56 2S	++	+	++	++++
779/780	Q305E	++	++	++	+
781/782	S114P/E206P/E283S/R289Q/I5 62S	++	++	++	++++
783/784	K56R	++	++	++	++
785/786	R289Q/I562S	++	++	++	++
¹ All activities were determined relative to reference polypeptide SEQ ID NO: 604. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; "+++" > 2; and "++++" > 3.					

EXAMPLE 9

TAL Variants of SEQ ID NO: 736

[0226] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 736 for improved tyrosine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 735, was carried out by constructing libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0227] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4 with the following conditions: 20 μ L of HTP lysate diluted 10-fold in water was assayed with 2.2 mM tyrosine for 5 min and 10 μ L of undiluted HTP lysate was assayed with 0.1 mM tyrosine for 5 min. The results of the assays are shown in Tables 9.1 and 9.2. SEQ ID NO: 790 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease

[0228] TAL variants were challenged with chymotrypsin and trypsin as described in Example 7, and residual activity was determined as described in Example 6. The results of this assay are shown in Tables 9-1 and 9-2.

HTP Activity Analysis of Clarified Lysates Pretreated with Acidic Buffer

[0229] TAL variants were challenged with acidic buffer as described in Example 8, and residual activity was determined as described in Example 7. The results of this assay are shown in Tables 9-1 and 9-2.

Table 9-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736) ¹				
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC
787/788	G549D	+	+	++
789/790	T49D/S59A/R289Q/I562S	+	++	+
791/792	S59A/E145V/H234Y/I291V	+	+	++
793/794	T49D/S59A/Q66N/R289Q	+	++	+
795/796	R56G/H234Y/I291V		+	+
797/798	R56G/S59A/Q111K/H234Y/N531D	+	+	++
799/800	T49D/Q111K/N531D	+	+	+
801/802	Q111K/I291V	+		+
803/804	K518Q/N531D/G549D/I562S	+	+	++
805/806	R56G/S59A/E145V/R289Q/K518Q/I562S	++	++	+
807/808	I291V/K518Q/G549D	+		++
809/810	R56G/S59A/H234Y	+	++	++
811/812	R56G/Q111K/E145V/H234Y/R289Q/N531D/I562S	+	+	++
813/814	K518Q	+	+	+
815/816	Q111K/E145V	+		++
817/818	T49D/R56G/Q66N/H234Y	+	++	+
819/820	H234Y	+	+	++
821/822	T49D/R56G/Q66N/Q111K/H234Y/I291V/K518Q	+	+	+
823/824	T49D/R56G/S59A/Q66N/I291V/N531D/G549D	+	+	++

Table 9-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736) ¹				
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC
825/826	Q111K/E145V/H234Y/I291V/I562S	+	+	++
827/828	Q111K/E145V/H234Y/I562S	+	+	++
829/830	T49D/R56G/S59A/Q111K/G549D	+	++	++
831/832	Q111K/R289Q	+	+	++
833/834	S59A	+	+	++
835/836	R56G/Q111K/K518Q/G549D	+	+	+
837/838	T49D/Q66N/Q111K/H234Y/I291V/K518Q/I562S	+	+	++
839/840	N531D	+	+	+
841/842	R56G/S59A/Q111K/I291V/K518Q/N531D	+		+
843/844	R56G/S59A/Q111K/E283D/K518Q/N531D	+	+	+
845/846	T49D/H234Y	+	+	++
847/848	S59A/H234Y/I291V	+	+	++
849/850	Q111K/H234Y	+	+	++
851/852	D20G/S59A/H234Y/K518Q/G549D/I562S		+	++
853/854	R56G/S59A/K518Q	+	+	+
855/856	R56G/S59A/Q111K/H234Y/R289Q	+	++	++
857/858	D20G/T49D/R56G/S59A/Q111K/I291V		+	
859/860	S59A/H234Y/I291V/I387T/G549D/I562S	+		+
861/862	T49D/S59A/Q66N/E145V/H234Y	+		
863/864	Q111K/K518Q	+	+	+
865/866	H234Y/K518Q/G549D	+	+	++
867/868	S59A/Q111K/	+	+	++
869/870	R56G/Q111K/E145V/H234Y/K518Q/G549D/I562S	+	+	++
871/872	R56G/S59A/H234Y/K518Q	+	+	++
873/874	R56G/S59A/Q111K/I291V	+	+	+
¹ All activities were determined relative to reference polypeptide SEQ ID NO: 736. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; "+++" > 2; and "++++" > 3.				

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
875/876	K33N/Q37A/K518V/S521D/S548K	++	++	++	++
877/878	Q37A/R103L/Q305E/I336V/E523D/A540R	++	++	++	+++
879/880	K33N/L46R/E523D	++	++	++	++
881/882	Q37A/R103L/Q305E/S521D/L541A/S548K	++	++	++	+++
883/884	Q37A/Q305E/I336V/A540R/S548K	++	+	++	+++
885/886	L46R/R103L/Q305E/S548K	++	+	++	+++
887/888	Q37A/R103L/L541A/S548K	++	++	++	+++
889/890	Q37A/I336V/A540R	++	++	++	+++
891/892	Q37A/S548K	++	++	++	++
893/894	K33N/L46R/I336V/S521D/E523D	++	++	++	++
895/896	K33N/Q37A/E523D/A540R/S548K	++	++	++	+++
897/898	L46R/R103L/Q305E/Q471Y/A540R/S548K	++	+	++	+++
899/900	E523D	++	++		++
901/902	K33N/L46R/K518V/S521D/S548K	++	++		++
903/904	K33N/Q37A/I336V/A540R/S548K	++	++	++	+++
905/906	L46R/Q305E/E523D/S548K	++	+	++	++
907/908	K33N/L46R	++	++	++	++
909/910	Q37A/L541A	+	++	+	++
911/912	K33N/L46R/Q305E/I336V	++	++	++	++
913/914	L46R/Q305E/I336V/K522E	++	+	++	++
915/916	L46R/R103L/Q305E	++	+	++	+++
917/918	K33N/Q37A/Q305E/A328Q/S548K	++	++	++	+++
919/920	L46R/Q305E/Q471Y	++	+	++	++
921/922	Q37A/Q305E/E523D/L541A/S548K	++	+	++	+++
923/924	Q37A/Q305E/L541A/S548K	++	+	++	++
925/926	L46R/I336V/E523D/S548K	++	++	++	++

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
927/928	K33N/Q37A/R103L/A519P/E523D	++	++	++	+++
929/930	K33N/L46R/S548K	++	++	++	++
931/932	K33N/L46R/L541A	++	++	++	++
933/934	Q37A/Q305E/Q471Y/A540R/S548K	++	+	++	++
935/936	Q37A/E523D/L541A	++	++	++	++
937/938	Q37A/I336V/Q471Y/L541A/S548K	+	++	++	++
939/940	K33N/L46R/R103L/Q305E/A540R	++	++	++	+++
941/942	K33N/Q37A/R103L/K518V/E523D/L541A	++	++	++	++
943/944	K33N/Q37A/Q471Y/E523D/A540R/S548K	++	++	++	++
945/946	K33N/Q37A/R103L/Q471Y/A519P/S548K	++	++	++	+++
947/948	L46R/R103L/Q305E/I336V/E523D	+	+	++	+++
949/950	Q37A/Q471Y/S521D/A540R/S548K	++	++	++	++
951/952	K33N/Q37A/S548K	++	++	++	++
953/954	Q37A/S521D/E523D/S548K	++	++	++	++
955/956	K33N/L46R/I336V/S521D	+	++	+	++
957/958	L46R/I336V/A540R/S548K	++	++	++	++
959/960	Q37A/Q305E/I336V/E523D/S548K	++	+	++	+++
961/962	K33N/Q37A/Q305E/I336V/S521D/S548K	++	++	++	+++
963/964	Q37A/Q305E/I336V/S521D/A540R/S548K	++	++	++	+++
965/966	K33N/Q37A/Q305E/A540R	++	++	++	+++
967/968	Q37A/Q305E/S548K	++	++	++	+++
969/970	Q37A/Q305E/Q471Y/E523D/A540R/S548K	++	+	++	++
971/972	K33N/Q37A/R103L/Q305E	++	++	++	+++
973/974	K33N/Q37A/I336V/A540R	++	++	++	+++
975/976	K33N/Q37A/K518V/S521D/A540R	++	++	++	++

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
977/978	K33N/Q37A/I336V	++	++	++	++
979/980	K33N/Q37A/Q305E/A328Q	++	++	++	++
981/982	Q37A/A540R/S548K	++	++	++	++
983/984	Q37A/I336V/S548K	++	++	++	++
985/986	L46R/R103L/L541A/S548K	++	++	++	+++
987/988	K33N/Q37A	++	++	++	++
989/990	Q37A/R103L/A519P/L541A/S548K	++	++	++	+++
991/992	Q37A/R103L/A328Q/S521D/L541A/S548K	++	++	++	+++
993/994	L46R/S521D/E523D	++	++	++	++
995/996	K33N/Q37A/R103L/Q305E/E523D/S548K	++	++	++	+++
997/998	L46R/R103L/Q305E/P520Q/A540R	++	+	++	+++
999/1000	L46R/Q305E/I336V/K518V	++	+	++	++
1001/1002	K33N/Q37A/R103L/Q305E/S548K	++	+	++	+++
1003/1004	Q37A/A519P	++	++	++	++
1005/1006	Q37A/Q471Y	++	++	++	++
1007/1008	L46R/Q305E	++	+	++	++
1009/1010	R103L	++	++	++	+++
1011/1012	L46R/E523D/L541A/S548K	++	++	++	++
1013/1014	K33N/Q37A/K518V/S548K	++	++	++	++
1015/1016	Q37A/Q471Y/K518V	++	++	++	++
1017/1018	K33N/L46R/R103L/A540R/S548K	++	++	++	+++
1019/1020	Q37A/S521D/A540R	++	++	++	++
1021/1022	K33N/L46R/R103L/Q305E/I336V/S548K	++	+	++	+++
1023/1024	L46R/Q305E/S548K	++	++	++	++
1025/1026	Q37A/Q305E/A519P/S548K	++	+	++	++
1027/1028	Q37A/I336V/S521D/E523D/S548K	++	++	++	+++
1029/1030	Q37A/E523D/S548K	++	++	++	++

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
1031/1032	K33N/Q37A/R103L/Q305E/I336V/L541A/S548K	++	++	++	++++
1033/1034	Q37A/R103L/Q305E/Q471Y/A540R/S548K	++	++	++	+++
1035/1036	K33N/Q37A/Q305E/L541A	++	++	++	++
1037/1038	Q37A/Q305E/I336V	++	++	++	+++
1039/1040	Q37A/Q305E/S521D/A540R	++	+	++	++
1041/1042	S521D/S548K	++	+	++	++
1043/1044	K33N/Q37A/R103L/A540R	++	++	++	+++
1045/1046	R103L/S521D/E523D/A540R	+	++	+	+++
1047/1048	K33N/L46R/I336V/A540R/S548K	++	++	++	+++
1049/1050	Q37A/I336V	++	++	++	++
1051/1052	K33N/Q37A/Q305E/Q471Y/S521D/S548K	++	++	++	++
1053/1054	K33N/L46R/Q305E	++	+	++	++
1055/1056	Q37A/R103L/A328Q/I336V/K518V/E523D/S548K	++	++	++	+++
1057/1058	L46R/R103L/Q305E/I336V/Q471Y/A540R/S548K	++	++	++	+++
1059/1060	K33N/L46R/R103L/Q305E/I336V/K518V/A519P/A540R	++	++	++	+++
1061/1062	L46R/S548K	++	++	++	++
1063/1064	Q37A/R103L	++	++	+	+++
1065/1066	Q37A/R103L/Q305E/Q471Y	++	++	++	+++
1067/1068	K33N/L46R/I336V/A540R	++	++	++	+++
1069/1070	Q37A/Q305E/L541A	++	+		++
1071/1072	L46R/Q305E/I336V/S548K	++	+	++	++
1073/1074	K33N/Q37A/S521D/S548K	++	++	++	++
1075/1076	Q37A	++	++	++	++
1077/1078	K33N/Q37A/Q305E/E523D/A540R	++	++	++	+++
1079/1080	L46R/Q305E/I336V	++	+	++	++

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
1081/1082	K33N/Q37A/R103L/I336V/K518V/L541A/S548K	++	++	++	+++
1083/1084	L46R	++	++	++	++
1085/1086	K33N/Q37A/A540R	++	++	++	+++
1087/1088	Q37A/R103L/A540R	++	++	++	+++
1089/1090	K33N/Q37A/Q305E	++	++	++	++
1091/1092	Q37A/R103L/I336V/S521D/L541A	+	++	+	+++
1093/1094	K33N/L46R/Q66K/Q305E/S521D/E523D/A540R/S548K		+	++	+++
1095/1096	K33N/Q37A/E523D	++	++	++	++
1097/1098	L46R/E523D/A540R	++	++	++	++
1099/1100	Q37A/R103L/Q305E/A540R	++	++	++	+++
1101/1102	K33N/Q37A/R103L	++	++	++	+++
1103/1104	L46R/S521D/S548K	++	++	++	++
1105/1106	Q37A/I336V/S521D/E523D	++	++	++	++
1107/1108	L46R/R103L/S548K	++	++	++	+++
1109/1110	Q37A/R103L/I336V	++	++	++	+++
1111/1112	L46R/L541A/S548K	++	++	+	++
1113/1114	Q37A/Q305E	++	++	++	++
1115/1116	Q37A/R103L/Q305E/I336V/S521D/E523D/A540R/S548K	++	+	++	+++
1117/1118	K33N/L46R/Q305E/K518V/A540R/S548K	++	+	++	++
1119/1120	L46R/I336V/S521D/E523D	++	++	++	++
1121/1122	K33N/Q37A/Q305E/I336V/S521D/E523D/S548K	++	++	++	++
1123/1124	Q305E/I336V/L541A/S548K	++	+	++	++
1125/1126	L46R/R103L/E523D/S548K	++	++	++	++
1127/1128	Q37A/Q305E/I336V/L541A/S548K	++	+	++	++
1129/1130	Q37A/R103L/Q305E/I336V	++	+	++	+++

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
1131/1132	K33N/Q37A/Q305E/I336V/K518V/E523D	++	+	++	++
1133/1134	L46R/R103L/L541A	++	++	+	+++
1135/1136	I336V/S548K	+	++	+	++
1137/1138	R103L/I336V/A519P/S548K	++	++	+	+++
1139/1140	Q37A/Q471Y/K518V/A519P/E523D	++	++	++	++
1141/1142	A519P/S548K	+	+	+	++
1143/1144	K33N/Q37A/Q305E/I336V/Q471Y/L541A	++	++	++	++
1145/1146	K33N/Q37A/L46R/Q305E	++	+	++	++
1147/1148	Q37A/Q305E/S521D/E523D/A540R/S548K	++	+	++	++
1149/1150	K33N/L46R/S521D/S548K	++	++	++	++
1151/1152	Q37A/Q305E/Q471Y	++	+	++	++
1153/1154	Q37A/I336V/E523D/S548K	+	+	+	++
1155/1156	Q37A/Q305E/S521D/L541A/S548K	++	+	++	++
1157/1158	K33N/R103L/I336V/K518V/S521D/S548K	++	++	++	++
1159/1160	K33N/Q37A/Q305E/I336V/L541A	++	+	++	++
1161/1162	K33N/Q471Y/E523D/L541A	++	++	++	++
1163/1164	L46R/R103L/A540R/S548K	+	+	+	++
1165/1166	K33N/Q37A/R103L/E523D	+	++	+	++
1167/1168	L46R/I336V/A540R	++	++	++	++
1169/1170	L46R/S521D/E523D/A540R	++	++	++	++
1171/1172	L46R/L541A	++	++	++	+
1173/1174	K33N/L46R/I336V/Q471Y/A519P/E523D/S548K	++	++	++	++
1175/1176	Q37A/A540R	++	++	++	++
1177/1178	L46R/T49D/N531D/G549D	+	+	+	++
1179/1180	R289Q/S521D/E523D	+	+	+	

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
1181/1182	H234Y/R289Q/E523D/N531D/G549D/I562S	+	+	+	+++
1183/1184	R289Q	+	+	+	+
1185/1186	S521D	+	+	+	+
1187/1188	L46R/T49D/Q111K/H234Y/I336V	+	+	+	+++
1189/1190	L46R/T49D/Q111K/H234Y/R289Q/L436V/G549D	+	+	+	++
1191/1192	L46R/T49D/H234Y/G549D	+	+	+	+++
1193/1194	T49D	+	+	+	
1195/1196	T49D/R289Q/Q305E/I336V/E523D	+	+	+	
1197/1198	T49D/Q111K/H234Y/R289Q/I336V/E523D/N531D/G549D	+	+	+	++
1199/1200	S59A/G549D	+	+	+	+++
1201/1202	T49D/S59A/H234Y/R289Q/I336V/E523D/N531D/G549D	+	+		++
1203/1204	L46R/H234Y/R289Q/G549S	+	+	+	+++
1205/1206	T49D/H234Y/R289Q/E523D	+	+	+	++
1207/1208	S59A/Q111K/R289Q	+	+	+	+++
1209/1210	R289Q/I336V/G549D	+	+	+	++
1211/1212	T49D/Q111K/H234Y	+	+	+	+++
1213/1214	T49D/H234Y/Q305E/G549D	+	+	+	+++
1215/1216	H234Y/S521D/E523D/G549D	+	+		++
1217/1218	L46R/T49D/R289Q/E523D/N531D/G549D/I562S	+	+	+	++
1219/1220	T49D/Q111K/E523D/N531D/G549D	++	+	+	++
1221/1222	T49D/H234Y/G549D	+	++	+	+++
1223/1224	T49D/H234Y/R289Q	+	++	+	++
1225/1226	L46R/Q111K/H234Y/R289Q/N531D/G549D	+	+	+	+++
1227/1228	Q111K/R289Q/I336V/S521D	+	+	+	++
1229/1230	T49D/H234Y	+	++	+	++

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
1231/1232	T49D/E523D/G549D	+	++	+	++
1233/1234	L46R/T49D/Q111K/H234Y/I336V/E523D/G549D	+	++	+	+++
1235/1236	T49D/Q111K/R289Q	+	++	+	+
1237/1238	T49D/S59A/Q111K/R289Q/E523D	+	++	+	++
1239/1240	H234Y/I562S	+	+	+	++
1241/1242	S59A/Q111K/H234Y/R289Q/Q305E/I336V/G549D	+	+	+	++++
1243/1244	L46R/S59A/G549D/I562S/	+	++	+	+++
1245/1246	T49D/Q111K/H234Y/I336V/S521D/E523D	+	+	+	++
1247/1248	H234Y/R289Q/N531D	+	+	+	++
1249/1250	H234Y/G549D	+	+	+	+++
1251/1252	H234Y/R289Q/G549D	+	+	+	+++
1253/1254	T49D/Q111K/H234Y/R289Q/S521D/E523D/N531D/G549D/I562S	+	+	+	++
1255/1256	H234Y/A540R	+	+	+	+++
1257/1258	T49D/Q111K/H234Y/I336V/E523D/N531D	+	+	+	++
1259/1260	H234Y/R289Q	+	+	+	++
1261/1262	T49D/S521D/G549D	+	++	+	++
1263/1264	R289Q/S521D/E523D/G549D	+	+	+	+++
1265/1266	T49D/S59A/Q111K/H234Y/R289Q/S521D	+	++	+	+++
1267/1268	T49D/R289Q/I336V/S521D/N531D	+	+	+	
1269/1270	T49D/S59A/S521D/N531D	+	+	+	++
1271/1272	Q111K/H234Y/R289Q	+	+	+	+++
1273/1274	L46R/R289Q/G549D	+	+	+	+++
1275/1276	T49D/S59A/H234Y/R289Q/I336V	+	+	+	++
1277/1278	H234Y/I336V/N531D/I562S	+	+	+	+++
1279/1280	T49D/I336V/S521D/I562S	+	+	+	+

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
1281/1282	L46R/Q111K/H234Y/S521D/G549D	+	+	+	+++
1283/1284	Q111K/S521D/E523D/G549D	+	+	+	+++
1285/1286	L46R/T49D/H234Y/I336V/S521D/E523D/G549D	+	+	+	+++
1287/1288	T49D/S59A/I336V	+	+	+	++
1289/1290	S521D/I562S	+	+	+	+
1291/1292	H234Y/R289Q/E523D/G549D	+	+	+	+++
1293/1294	L46R/T49D/H234Y/R289Q/I336V	+	+	+	++
1295/1296	T49D/S521D/N531D/G549D/I562S	+	+	+	++
1297/1298	T49D/Q111K/H234Y/G549D	+	++	+	+++
1299/1300	S59A/Q111K/I336V	+	+	+	+++
1301/1302	L46R/T49D/S59A/Q111K/E523D/N531D/G549D	+	+	+	+++
1303/1304	L46R/T49D/Q111K/I336V/G549D	+	+	+	+++
1305/1306	T49D/H234Y/R289Q/I336V/N531D/G549D	+	+	+	++
1307/1308	Q111K/H234Y/R289Q/E523D	+	+	+	+++
1309/1310	L46R/T49D/Q111K/H234Y/R289Q/N531D/G549D	+	+	+	+++
1311/1312	L46R/H234Y/G549D	+	+	+	+++
1313/1314	S59A	+	+	+	++
1315/1316	T49D/H234Y/R289Q/E523D/N531D/A540R	+	+	+	++
1317/1318	T49D/S59A/R289Q/I336V	+	++	+	++
1319/1320	T49D/Q111K/H234Y/R289Q/E523D/G549D	+	++	+	++
1321/1322	L46R	+	+	+	+
1323/1324	R289Q/S521D/E523D/A540R	+	+	+	+
1325/1326	G549D	+	+	+	++
1327/1328	L46R/Q111K/E523D/N531D/G549D	+	+	+	++
1329/1330	T49D/S59A/R289Q/Q305E/I336V	++	+	+	++

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
1331/1332	L46R/S59A/H234Y	+	+	+	+++
1333/1334	T49D/G549D	+	++	+	++
1335/1336	H234Y/N531D/G549D	+	+	+	+++
1337/1338	T49D/Q111K/H234Y/E523D/N531D/G 549D	+	+	+	+++
1339/1340	T49D/R289Q/I336V	+	+	+	
1341/1342	S59A/Q111K/H234Y/R289Q/Q305E/G5 49D	+	+	+	++++
1343/1344	N531D/G549D	+	+	+	++
1345/1346	Q111K/R289Q/I336V/E523D/G549D	+	+	+	+++
1347/1348	H234Y/R289Q/I336V/E523D	+	+	+	++
1349/1350	H234Y/I336V	+	+	+	++
1351/1352	A540R	+	+	+	+
1353/1354	T49D/Q111K/H234Y/N531D	+	+	+	++
1355/1356	H234Y	+	+	+	++
1357/1358	T49D/Q111K	+	+	+	+
1359/1360	T49D/Q111K/N531D/G549D	+	+	+	++
1361/1362	L46R/G549D	+	+	+	++
1363/1364	Q111K/I336V/I562S	+	++	+	++
1365/1366	H234Y/E523D/N531D	+	+	+	++
1367/1368	T49D/H234Y/R289Q/E523D/G549D	+	++	+	++
1369/1370	T49D/Q111K/R289Q/I336V/S521D/G5 49D	+	++	+	++
1371/1372	T49D/H234Y/S521D	+	+	+	++
1373/1374	L46R/T49D/H234Y/A540R/G549D	+	+	+	+++
1375/1376	L46R/S521D/E523D/G549D	+	+	+	++
1377/1378	S521D/G549D	+	+	+	++
1379/1380	L46R/H234Y/S521D/E523D/N531D/A5 40R/G549D	+	+	+	+++
1381/1382	R289Q/E523D	+	+	+	+

Table 9-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 736) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 736)	2 mM Tyr FIOPC	Protease FIOPC	0.1 mM Tyr FIOPC	pH 4 FIOPC
1383/1384	H234Y/S521D/E523D	+	+	+	++
¹ All activities were determined relative to reference polypeptide SEQ ID NO: 736. Levels of increased activity are defined as follows: "+"= 0.9 to 1.2; "++" > 1.2; "+++" > 2; and "++++" > 3.					

EXAMPLE 10

TAL Variants of SEQ ID NO: 790

[0230] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 790 for improved tyrosine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 790 was carried out by constructing libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0231] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4 with the following conditions: 20 μ L of HTP lysate diluted 10-fold in water was assayed with 2.2 mM tyrosine for 5 min. The results of the assays are shown in Tables 10-1 and 10-2. SEQ ID NO: 1454 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease and/or Acidic Buffer

[0232] TAL variants were challenged with chymotrypsin and trypsin, whereby 50 μ L of HTP lysate diluted 2-fold was incubated with 50 μ L 4 g/L protease mix for 2 h at 37°C in a THERMOTRON[®] (INFORS) titre-plate shaker (400 rpm). Protease mix consisted of 4 mg/mL chymotrypsin (Sigma Aldrich) and 4 mg/mL trypsin (Sigma Aldrich) in 100 mM sodium phosphate pH 8.0. Residual activity was determined by adding 40 μ L of the protease-treated lysate to 160 μ L of 200 mM sodium phosphate, 2.5 mM tyrosine, pH 7.0, in a 96-well UV-STAR[®] plate (Greiner Bio-One). The reactions were mixed briefly, and activity was determined as described in Example 4. The results of this assay are shown in Tables 10-1 and 10-2.

[0233] TAL variants were challenged with acidic buffer, whereby 90 μ L of heat-treated clarified lysate was incubated with 90 μ L McIlvaine buffer pH 4 for 1-2 h at 37°C in a THERMOTRON[®]

(INFORS) titre-plate shaker (400 rpm). After incubation, the lysate solutions were briefly centrifuged, and residual activity was determined by adding 20 μ L of the acidic buffer-treated lysate to 180 μ L of 200 mM sodium phosphate, 2.5 mM tyrosine, pH 7.0, in a 96-well UV-STAR[®] plate (Greiner Bio-One). The reactions were mixed briefly, and activity was determined as described in Example 4. The results of this assay are shown in Tables 10-1 and 10-2.

[0234] In some instances, the acidic buffer-treated lysate described above was further challenged with protease in a combined pH and protease assay. After pretreatment with acidic buffer, the lysate solutions were briefly centrifuged, and 75 μ L of the supernatant was incubated with 75 μ L 4 g/L protease mix dissolved in 200 mM sodium phosphate dibasic for 2 h at 37°C in a THERMOTRON[®] (INFORS) titre-plate shaker (400 rpm). Residual activity was determined by adding 40 μ L of the pretreated lysate to 160 μ L of 200 mM sodium phosphate, 2.5 mM tyrosine, pH 7.0, in a 96-well UV-STAR[®] plate (Greiner Bio-One). The reactions were mixed briefly, and activity was determined as described in Example 4. The results of this assay are shown in Table 10-1.

Table 10-1. Relative Activity of TAL Variants on Tyrosine under various conditions (Relative to SEQ ID NO: 790)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 790)	2 mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1385/1386	L202R/K332Q/D408E	++	++	++	+
1387/1388	K44R	+	+	+	+
1389/1390	D408E	++	++	+	+
1391/1392	I24T/L202R/G351N	+	++	+	++
1393/1394	I24T/K44R/R464Q	+	++	+	+
1395/1396	I24T/K201N/L202R/G351N/Q507R	+	++	+	++
1397/1398	L202R	+	++	+	+
1399/1400	K33N/Q37A/Q111K/S548K	+	++	+	+
1401/1402	K33N/R56G/R103L/Q111K	+	++	+	+
1403/1404	L46R/I336V/A540R/G549D	+	++	++	++
1405/1406	K33N/I336V/G549D	+	++	+	+
1407/1408	K33N/I336V/A540R/S548K	+	+	+	+
1409/1410	K33N/Q37A/L46R/R103L/Q111K/H234Y	+	++	++	++
1411/1412	Q37A/L46R/R56G/E523D	+	++	+	+
1413/1414	K33N/I336V	+	++	+	+
1415/1416	K33N/Q37A/E523D/A540R/S548K	++	++	+	+

Table 10-1. Relative Activity of TAL Variants on Tyrosine under various conditions (Relative to SEQ ID NO: 790)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 790)	2 mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1417/1418	K33N/Q37A/L46R/Q111K/I336V/A540R	+	+	++	++
1419/1420	K33N/L46R/R56G/H234Y/A248V/G549D	+	++	+	++
1421/1422	K33N/R103L/Q111K/H234Y	+	++	+	+
1423/1424	K33N/Q37A/L46R/R56G/R103L/E523D/A540R/S548K/G549D	+	++	+	++
1425/1426	K33N/Q37A/L46R/R56G/Q111K/H234Y/E523D	+	++	+	++
1427/1428	K33N/Q37A/L46R/R103L/Q111K/S548K/G549D	+	++	+	++
1429/1430	Q37A/L46R/H234Y	+	++	++	++
1431/1432	L46R/H234Y/A540R/S548K	+	+	+	++
1433/1434	Q37A/Q111K/E523D	+	++	+	+
1435/1436	K33N/L46R	+	++	+	++
1437/1438	K33N/L46R/R103L/E523D/G549D	+	++	++	++
1439/1440	K33N/H234Y/I336V/E523D/A540R/S548K/G549D	+	++	+	++
1441/1442	Q37A/R56G/H234Y/I336V/E523D/A540R/S548K/G549D	+	+++	+	++
1443/1444	K33N/Q111K/H234Y/S548K	+	++	+	++
1445/1446	K33N/R103L/Q111K/H234Y/I336V/E523D/S548K	+	++	+	++
1447/1448	K33N/R103L/Q111K/I336V	+	++	+	+
1449/1450	H234Y/E523D/A540R/S548K/G549D	+	++	++	++
1451/1452	K33N/H234Y/E523D/S548K	+	++	+	++
1453/1454	K33N/Q37A/H234Y/I336V/E523D/S548K	+	++	+	+
1455/1456	Q37A/L46R/I336V/E523D/A540R/S548K	+	++	++	++

Table 10-1. Relative Activity of TAL Variants on Tyrosine under various conditions (Relative to SEQ ID NO: 790)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 790)	2 mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1457/1458	Q37A/I336V	+	++	+	+
1459/1460	Q37A	+	++	+	+
1461/1462	Q37A/L46R/I336V/A540R/S548K		+	+	++
1463/1464	K33N/Q37A/R56G/Q111K/H234Y/E523D/A540R/S548K	+	++	+	++
1465/1466	K33N/Q37A/L46R/I336V	+	++	+	++
1467/1468	E523D/S548K	+	+	+	+
1469/1470	K33N/Q37A/R56G/H234Y/E523D/A540R/S548K	+	++	+	++
1471/1472	L46R/R103L/A328Q/I336V/E523D	+	++	++	++
1473/1474	K33N/Q37A/Q111K/E523D/A540R	+	++	+	+
1475/1476	K33N/L46R/R56G/Q111K/S548K	+	++	+	++
1477/1478	K33N/H234Y/A540R/S548K/G549D	+	++	++	++
1479/1480	Q37A/S548K/G549D	+	++	+	++
1481/1482	K33N/H234Y/E523D/A540R/S548K	+	++	++	++
1483/1484	K33N/Q37A/L46R/R56G/Q111K/E523D/A540R	+	++	+	++
1485/1486	K33N/Q37A/L46R/S548K/G549D	+	++	++	++
1487/1488	K33N/Q37A/L46R/Q111K/H234Y/A328Q/E523D/A540R/S548K	+	++	++	++
1489/1490	I336V/E523D	+	++	+	+
1491/1492	K33N/Q37A/R103L/Q111K/H234Y/I336V/A540R/S548K	+	++	+	++
1493/1494	L46R/H234Y/I336V	++	++	++	++
1495/1496	K33N/R103L/Q111K/H234Y/A540R/G549D	+	++	+	++
1497/1498	K33N/Q37A/Q111K/H234Y/E523D/A540R/S548K	+	++	+	++
1499/1500	Q37A/R103L/I336V/S548K/G549D	+	++	+	++

Table 10-1. Relative Activity of TAL Variants on Tyrosine under various conditions (Relative to SEQ ID NO: 790)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 790)	2 mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1501/1502	Q37A/H234Y/A328Q/I336V/E523D	+	++	+	+
1503/1504	K33N/H234Y/A328Q/E523D/A540R/G549D	+	++	+	++
1505/1506	K33N/Q37A/L46R/H234Y/E523D	+	++	++	++
1507/1508	K33N/I336V/E523D/A540R/S548K/G549D	+	++	++	++
1509/1510	L46R/R103L/I336V	+	++	++	++
1511/1512	K33N/Q37A/L46R/R103L/E523D	+	++	++	++
1513/1514	K33N/Q37A/R103L/I336V/E523D/A540R/S548K	+	++	+	++
1515/1516	Q37A/R56G/I336V/E523D/A540R/S548K	+	++	+	++
¹ All activities were determined relative to the reference polypeptide of SEQ ID NO: 790. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; and "+++" > 2					

Table 10-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 790)¹				
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 790)	2 mM tyr FIOPC	Protease FIOPC	pH 4 FIOPC
1517/1518	S424A	+		
1519/1520	M102P		+++	+
1521/1522	G417A	++	++	+
1523/1524	L418V	++	+	+
1525/1526	I420L	+	+	+
1527/1528	S402A	+	++	+
1529/1530	T391N	+	++	+
1531/1532	M392A	+	+	+
1533/1534	L313M	++	+	+
1535/1536	L210T	++	++	+
1537/1538	D530V	++	++	+

Table 10-2. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 790) ¹				
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 790)	2 mM tyr FIOPC	Protease FIOPC	pH 4 FIOPC
1539/1540	L313I	++	++	++
1541/1542	I74A	++	++	+
1543/1544	L415F	++		+
1545/1546	R506C	+	+	+
¹ All activities were determined relative to the reference polypeptide of SEQ ID NO: 790. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; and "+++" > 2.				

EXAMPLE 11

TAL Variants of SEQ ID NO: 1454

[0235] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 1454 for improved tyrosine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 1454 was carried out by constructing libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0236] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4 with the following conditions: 20 µL of HTP lysate diluted 10-fold in water was assayed with 2.2 mM tyrosine for 5 min. The results of the assays are shown in Table 11-1, and SEQ ID NO: 1578 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease and/or Acidic Buffer

[0237] TAL variants were challenged with chymotrypsin and trypsin as described in Example 10. Residual activity was determined as described in Example 10, and the results of this assay are shown in Table 11-1.

[0238] TAL variants were challenged with acidic buffer, whereby 50 µL of heat-treated clarified lysate was incubated with 50 µL McIlvaine buffer pH 3.8 for 1.5 h at 37°C in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm). After incubation, the lysate solutions were briefly centrifuged, and residual activity was determined by adding 40 µL of the acidic buffer-treated lysate to 160 µL of 200 mM sodium phosphate, 2.5 mM tyrosine, pH 7.0, in a 96-well UV-STAR® plate (Greiner Bio-

One). The reactions were mixed briefly, and activity was determined as described in Example 10. The results of this assay are shown in Table 11-1.

[0239] In some instances, acidic buffer-treated lysate was further challenged with protease in a combined pH and protease assay. After 30 μ L of heat-treated clarified lysate was incubated with 30 μ L McIlvaine buffer pH 3.8 for 1.5 h at 37°C, 60 μ L 4 g/L protease mix dissolved in 200 mM sodium phosphate dibasic was added, and the resulting solution was incubated for 2 h at 37°C in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm). Residual activity was determined as described in Example 10, and the results of this assay are shown in Table 11-1.

Table 11-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1454) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1454)	2 mM Tyr FIOPC	Protease FIOPC	pH 3.8 FIOPC	Combined pH and Protease FIOPC
1547/1548	I24T/K44R/G549D		++	++	+
1549/1550	I24T/L46R/Q111K/R506C	+	++	++	+
1551/1552	I24T/K44R/L46R/L202R/T391N		++	++	+
1553/1554	Q111K/L202R/L313M/G417A/A540R/G549D	+	++	+++	+
1555/1556	K44R/R103L/Q111K/L313M/T391N/A540R		++	++	+
1557/1558	L313M/T391N/A540R/G549D		++		+
1559/1560	I24T/K44R/L202R/L313M/T391N/A540R		++	++	+
1561/1562	I24T/L46R/R103L/T391N/R506C		++	++	+
1563/1564	K44R/L46R/R103L/Q111K/T391N		++	++	+
1565/1566	Q111K/L202R/T391N		++	++	+
1567/1568	I24T/K44R/Q111K/L202R/R464Q/R506C	+	+	++	+
1569/1570	L202R/L313M/T391N/G549D		++	++	+
1571/1572	L46R/Q111K/R506C	+	++	++	+
1573/1574	L202R/R506C/A540R/G549D		+	+++	+
1575/1576	R103L/L313M/G549D	+	+	+	++
1577/1578	I24T/L46R/M102P/L313M/R506C	+	++	++	++
1579/1580	I24T/L202R	+	++	++	+

Table 11-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1454)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1454)	2 mM Tyr FIOPC	Protease FIOPC	pH 3.8 FIOPC	Combined pH and Protease FIOPC
1581/1582	Q111K/L202R/L313M/T391N/R506C	+	++	++	+
1583/1584	I24T/L46R/R103L/Q111K/R464Q/R506C/G549D	+	++	+++	++
1585/1586	G417A	+	++	+	+
1587/1588	L202R/R506C/A540R	+	+	+++	+
1589/1590	Q111K	+	++	+	++
1591/1592	I24T	+	++	+	+
1593/1594	I24T/L46R/Q111K/L313M/T391N		+	++	+
1595/1596	Q111K/L202R/L313M/T391N/R464Q	+	++	++	+
1597/1598	L46R/R103L/R506C	+	+	+++	+
1599/1600	L202R/G417A/R464Q/A540R/G549D	+	++	+++	++
1601/1602	K44R/L46R/R103L/L202R/L313M/T391N	+	++	++	++
1603/1604	I24T/R103L/L202R	+	++	+++	++
1605/1606	I24T/L46R/L202R/T391N/R506C		++	+	+
1607/1608	I24T/L46R/G549D	+	++	+++	++
1609/1610	K44R/L46R/R103L/L202R/G417A/R464Q	+	+	++	+
1611/1612	L46R/L313M/T391N/A540R	+	++	++	+
1613/1614	L46R/L202R/R506C/G549D		+	+++	+
1615/1616	Q111K/L202R/T391N/A540R		++	++	+
1617/1618	K44R/Q111K/R464Q/R506C	+	+	++	+
1619/1620	Q111K/L202R	++	++	+++	++
1621/1622	I24T/K44R	+	+	++	+
1623/1624	L202R/R464Q/R506C	+	++	++	+
1625/1626	L46R/Q111K/G417A	+	++	++	+
1627/1628	L46R/L202R	+	++	+++	++

Table 11-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1454) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1454)	2 mM Tyr FIOPC	Protease FIOPC	pH 3.8 FIOPC	Combined pH and Protease FIOPC
1629/1630	I24T/L46R/Q111K/L313M/G549D	+	+	+++	++
1631/1632	Q111K/R464Q/A540R/G549D	+	++	+	++
1633/1634	K44R/L46R/M102P/L202R/L313M/G417A	+	++	++	++
¹ All activities were determined relative to the reference polypeptide SEQ ID NO: 1454. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; and "+++" > 2					

EXAMPLE 12

TAL Variants of SEQ ID NO: 1578

[0240] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 1578, for improved tyrosine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 1578 was carried out by constructing libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0241] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4, with the following conditions: 20 μ L of HTP lysate diluted 8-fold in water was assayed with 2.2 mM tyrosine for 5 min. The results of the assays are shown in Table 12-1. Based on the results, SEQ ID NO: 1660 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease and/or Acidic Buffer

[0242] TAL variants were challenged with chymotrypsin and trypsin as described in Example 10. The residual activity was determined as described in Example 10. The results of this assay are shown in Table 12-1.

[0243] TAL variants were challenged with acidic buffer, whereby 70 μ L of heat-treated clarified lysate was incubated with 70 μ L McIlvaine buffer pH 4 for 1.5 h at 37°C in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm). The residual activity was determined as described in Example 10. The results of this assay are shown in Table 12-1.

[0244] In some instances, acidic buffer-treated lysate was further challenged with protease in a combined pH and protease assay. Specifically, lysate challenged with acidic buffer as described above was centrifuged, and 50 μ L of the supernatant was incubated with 50 μ L 4 g/L protease mix dissolved in 100 mM sodium phosphate pH 8. The resulting solution was incubated for 2 h at 37°C in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm), and the residual activity was determined as described in Example 10. The results of this assay are shown in Table 12-1.

Table 12-1. Relative Activity of TAL Variants on Tyrosine under Various Conditions (Relative to SEQ ID NO: 1578)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1578)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1635/1636	D20G/K44R/L202R/C506R	++	++	++	++
1637/1638	R103L/L202R/A540R	++	++	++	++
1639/1640	Q111K	++	++	++	++
1641/1642	R103L/R464Q/G549D	+	++	+	++
1643/1644	Q111K/C506R	++	++	++	++
1645/1646	K44R/L202R/R464Q/C506R	++	++	++	++
1647/1648	R464Q/C506R	++	++	++	++
1649/1650	Q111K/L202R/M313L/Q471Y/C506R	++	++	++	++
1651/1652	C506R	++	++	++	++
1653/1654	R103L/Q471Y	++	++	+	++
1655/1656	M313L/R464Q/Q471Y/C506R	+	++	+	++
1657/1658	L202R/R464Q/C506R	++	++	++	++
1659/1660	L202R/R464Q/C506R/G549D	++	++	++	++
1661/1662	R103L/Q111K/Q471Y	++	++	+	++
1663/1664	R56G/Q111K/C506R	++	++	++	++
1665/1666	C506R/G549D	+	++	++	++
1667/1668	R103L/Q111K/L202R/R464Q/Q471Y	++	++	++	++
1669/1670	D20G/L202R/M313L/Q471Y/C506R	++	++	++	++
1671/1672	L202R	++	++	++	++
1673/1674	Q111K/L202R/Q471Y	++	++	++	++
1675/1676	R56G/C506R	++	++	++	++

Table 12-1. Relative Activity of TAL Variants on Tyrosine under Various Conditions (Relative to SEQ ID NO: 1578)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1578)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1677/1678	K44R/Q111K/L202R/R464Q/Q471Y/C506R/G549D	++	++	++	++
1679/1680	D20G/R103L/Q111K/Q471Y/C506R	++	++	++	++
1681/1682	L202R/M313L/R464Q/Q471Y/C506R	++	++	++	++
1683/1684	Q111K/L202R/M313L/L316Q	++	++	+	+
1685/1686	T24S	++	++	++	++
1687/1688	R504A	++	++	++	++
1689/1690	Y41L	++	++	++	++
1691/1692	R464S	++	++	++	++
1693/1694	A540R	++	++	++	++
1695/1696	Y41N	++	++	++	++
1697/1698	R464N	++	++	++	++
1699/1700	R504L	++	++	++	++
1701/1702	Y41H	++	++	+	++
1703/1704	Q66K	++	++	++	++
1705/1706	E51H	++	++	++	++
1707/1708	Q305E	++	++	++	++
1709/1710	R46S	++	++	++	++
1711/1712	A59S	++	++	++	++
1713/1714	K44E	++	++	++	++
1715/1716	Q66T	++	++	++	++
1717/1718	T24K	++	++	++	++
1719/1720	Q305D	++	++	++	++
1721/1722	Y41S	++	++	+	++
1723/1724	K44R	++	++	++	++
1725/1726	Y41Q	++	++	+	++
1727/1728	T48A	++	++	+	+
1729/1730	D523H	++	++	++	++

Table 12-1. Relative Activity of TAL Variants on Tyrosine under Various Conditions (Relative to SEQ ID NO: 1578)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1578)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1731/1732	Q66N	++	++	++	++
1733/1734	A36S	++	++	++	+
1735/1736	A59N	++	++	++	+
1737/1738	K50M	++	++	++	++
1739/1740	K44S	++	++	++	+
1741/1742	A519P	++	++	++	++
1743/1744	A519E	++	++	++	+
1745/1746	D27S	++	++	++	+
1747/1748	A36T	++	++	++	+
1749/1750	A519K	++	++	++	++
1751/1752	K44P	++	++	++	++
1753/1754	T24E	++	++	++	++
1755/1756	K518S	++	++	++	++
1757/1758	C500L	++	++	++	++
1759/1760	T48G	++	++	+	+
1761/1762	A540H	++	++	++	++
1763/1764	L208M	++	++	++	++
1765/1766	Q66H/W528R	++	++	++	++
1767/1768	T547G	++	++	++	++
1769/1770	A519T	++	++	++	+
1771/1772	Y41A	++	++	+	++
1773/1774	T24Q	++	++	+	++
1775/1776	R46A	++	++	+	+
1777/1778	Q55S	++	++	++	++
1779/1780	E51A	++	++	++	++
1781/1782	P197V	++	++	+	++
1783/1784	N33E	++	++	++	++
1785/1786	T547M/V553I	++	++	++	++
1787/1788	P272A	++	++	++	++
1789/1790	A331G	++	++	++	++

Table 12-1. Relative Activity of TAL Variants on Tyrosine under Various Conditions (Relative to SEQ ID NO: 1578)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1578)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1791/1792	A543T	++	++	++	++
1793/1794	A543V	++	++	++	++
1795/1796	I556L	++	++	++	++
1797/1798	A555S	++	++	++	++
1799/1800	Q470I	++	++	++	++
1801/1802	V559Y	++	++	++	++
1803/1804	Q289L	++	++	++	++
1805/1806	K332N	++	++	++	++
1807/1808	R292L/V553S	+	++	+	+
1809/1810	Q470T	++	++	++	++
1811/1812	Y432L	++	++	++	++
1813/1814	S435T	++	++	++	++
1815/1816	C506E	++	++	++	++
1817/1818	V559C	++	++	++	++
1819/1820	I556V	++	++	++	++
1821/1822	V559I	++	++	++	++
1823/1824	V559H	++	++	++	++
1825/1826	V559M	++	++	++	++
1827/1828	Y432T	++	++	++	++
1829/1830	V559L	++	++	++	++
1831/1832	S312C/V559Y	++	++	++	++
1833/1834	S435A	++	++	++	++
¹ All activities were determined relative to the reference polypeptide of SEQ ID NO: 1578. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; and "++" > 1.2.					

EXAMPLE 13

TAL Variants of SEQ ID NO: 1660

[0245] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 1660, for improved tyrosine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 1660 was carried out by constructing

libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0246] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4, with the following conditions: 20 μ L of HTP lysate diluted 8-fold in water was assayed with 2.2 mM tyrosine for 5 min. The results of the assays are shown in Table 13-1. Based on the results, SEQ ID NO: 1844 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease and/or Acidic Buffer

[0247] TAL variants were challenged with chymotrypsin and trypsin, whereby 50 μ L of HTP lysate diluted 2 or 2.5-fold was incubated with 50 μ L 4 g/L protease mix for 2 h at 37°C, in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm). Protease mix consisted of 4 mg/mL chymotrypsin (Sigma Aldrich) and 4 mg/mL trypsin (Sigma Aldrich) in 100 mM sodium phosphate pH 8.0. Residual activity was determined as described in Example 10. The results of this assay are shown in Table 13-1.

[0248] TAL variants were challenged with acidic buffer as described in Example 12. Residual activity was determined as described in Example 10. The results of this assay are shown in Table 13-1.

[0249] In some instances, acidic buffer-treated lysate was further challenged with protease in a combined pH and protease assay, as described in Example 12. Residual activity was determined as described in Example 10. The results of this assay are shown in Table 13-1.

Table 13-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1660) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1660)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1835/1836	A36S/P197V/Q305D/K332N/C500 L	++	++	++	++
1837/1838	Q305D/K332N/G457S/C500L	++	++	++	++
1839/1840	A36S/Q55S/Q305D/K332N/P410M	+++	++	++	++
1841/1842	A36S/P197V/Q305D/K332N/P410 M	++	++	++	++
1843/1844	A36S/Q305D/K332N/P410M	+++	++	++	++

Table 13-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1660)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1660)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1845/1846	A36S/Q305D/P410M	++	++	++	++
1847/1848	A36S/P197V/Q305D/K332N/P410M/V559I	++	++	++	++
1849/1850	Q305D/K332N/P410M	+++	++	++	++
1851/1852	Q305D	++	++	++	++
1853/1854	A36S/Q66N/P197V/Q305D/K332N/G457S	++	++	++	++
1855/1856	Q55S/Q305D/K332N/G457S/A543V/T547G	++	++	++	++
1857/1858	Q66N/Q305D/K332N	++	++	++	++
1859/1860	A36S/P197V/Q305D/P410M	++	++	++	++
1861/1862	Q305D/C500L/A543V/T547G	++	++	++	++
1863/1864	Q305D/K332N/P410M/C500L	+++	++	+++	++
1865/1866	P197V/Q305D	++	++	++	++
1867/1868	A36S/Q66N/P197V/Q305D/P410M	+++	++	++	++
1869/1870	A36S/P197V/Q305D	++	++	++	++
1871/1872	A36S/Q66N/Q305D/K332N/P410M	+++	++	+++	++
1873/1874	P197V/Q305D/P410M	+++	++	+++	++
1875/1876	Q305D/K332N	++	++	++	++
1877/1878	A36S/P197V/Q305D/C500L	++	+++	++	++
1879/1880	A36S/Q305D/K332N	++	++	++	++
1881/1882	A36S/Q66N/Q305D/C500L	++	++	++	++
1883/1884	Q55S/Q305D/C500L/V559I	++	++	++	++
1885/1886	Q305D/K332N/C500L	++	++	++	++
1887/1888	P197V/Q305D/K332N/P410M	+++	++	++	++
1889/1890	Q305D/P410M	+++	++	+++	++
1891/1892	A36S/P197V/Q305D/K332N/P410M/C500L	+++	++	+++	++
1893/1894	Q55S/Q305D	++	++	++	++
1895/1896	A36S/Q305D	++	++	++	++

Table 13-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1660)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1660)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1897/1898	P197V/Q305D/K332N/C500L/A54 3V/T547G	++	++	++	++
1899/1900	Q66N/Q305D	++	++	++	++
1901/1902	A36S/Q66N/Q305D	++	++	++	++
1903/1904	P197V/Q305D/C500L	++	++	++	++
1905/1906	S134C/R202L/Q305D	++	++	++	++
1907/1908	Q305D/K332N/G457S/A555S	++	++	++	+
1909/1910	Q305D/K332N/G457S	++	++	++	++
1911/1912	P272A/S435T/Y526L	++	++	++	++
1913/1914	L208M/P272A/Y432L	++	++	++	+
1915/1916	R46S/Q111K/L208M/P272A/S435 T/Y526L	++	++	++	++
1917/1918	Q111K/P272A/Q471Y/Y526L	++	++	++	++
1919/1920	L208M	++	++	++	++
1921/1922	Q111K/P272A/Y432T/S435T	++	++	++	++
1923/1924	Y432L/Y526L	++	++	++	++
1925/1926	D20G/P197V/Y432T/A519K	++	++	++	++
1927/1928	K44E/R46S/Q111K/L208M	++	++	++	++
1929/1930	Q111K/Y526L	++	+	++	+
1931/1932	Q111K	+	+	+	+
1933/1934	S435T	+	+	+	+
1935/1936	Q471Y	+	+	+	+
1937/1938	R46S/Y432L/Q471Y	+	+	+	+
1939/1940	K44E/R46S/Q111K/Y432T/A519K	+	+	+	+
1941/1942	Q111K/P272A/A519K	+	+	+	+
1943/1944	L208M/P410M/S435T	++	+	++	++
1945/1946	Y41L/Y432T/Y526L	++	++	++	+
1947/1948	T24E/R46S/P410M/S435T/K518S	++	++	++	++
1949/1950	D20G	++	++	++	++
1951/1952	L208M/S435T/A519K	++	++	++	++

Table 13-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1660) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1660)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1953/1954	S435T/A519K/Y526L	++	++	++	++
1955/1956	R46S/L208M/P272A/Y432L/S435 T/Y526L	++	++	++	++
1957/1958	P272A	++	++	+	++
1959/1960	K44E/Q111K/Y432L/A519K/Y526 L	++	++	++	++
1961/1962	D20G/K44E/L208M/P272A/A519 K	+	++	+	+
1963/1964	T24E	+	++	+	+
1965/1966	D20G/Q111K/L208M/P272A/P410 M/Y432T	++	++	++	++
1967/1968	Q111K/Y432T/Y526L	++	++	++	+++
1969/1970	Q471Y/Y526L	++	++	++	++
1971/1972	A519K	++	++	++	++
1973/1974	K44E/L208M/Y432T/S435T	++	++	++	++
1975/1976	S435T/K518S	++	++	++	++
1977/1978	Q111K/Y432L/S435T	++	++	+	++
1979/1980	Y41L/K44E/R46S/Q111K/P272A	++	++	++	+
1981/1982	L211Q/P410I	+	+	+	+
1983/1984	S298G/P410I	++	++	++	+
1985/1986	P410L	+	+	+	+
¹ All activities were determined relative to the reference polypeptide of SEQ ID NO: 1660. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; and "+++" > 2.					

EXAMPLE 14

TAL Variants of SEQ ID NO: 1844

[0250] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 1844, for improved tyrosine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 1844 was carried out by constructing

libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0251] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4, with the following conditions: 20 μ L of HTP lysate diluted 10-fold in water was assayed with 2.2 mM tyrosine for 5 min. The results of the assays are shown in Table 14-1. Based on the results, SEQ ID NO: 2030 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease and/or Acidic Buffer

[0252] TAL variants were challenged with chymotrypsin and trypsin, whereby 50 μ L of HTP lysate diluted 2.5-fold was incubated with 50 μ L 4 g/L protease mix for 2 h at 37°C in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm). Protease mix consisted of 4 mg/mL chymotrypsin (Sigma Aldrich) and 4 mg/mL trypsin (Sigma Aldrich) in 100 mM sodium phosphate pH 8.0. Residual activity was determined as described in Example 10. The results of this assay are shown in Table 14-1.

[0253] TAL variants were challenged with acidic buffer as described in Example 12. Residual activity was determined as described in Example 10. The results of this assay are shown in Table 14-1.

[0254] In some instances, acidic buffer-treated lysate was further challenged with protease in a combined pH and protease assay. Specifically, lysate challenged with acidic buffer as described above was centrifuged, and 40 μ L of the supernatant was incubated with 60 μ L 4 g/L protease mix dissolved in 100 mM sodium phosphate pH 8. The resulting solution was incubated for 2 h at 37°C, in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm), and residual activity was determined as described in Example 10. The results of this assay are shown in Table 14-1.

Table 14-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1844) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1844)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1987/1988	Q111K/Q289L	+++	+++	++	+++
1989/1990	Q289L/R504A	+++	+++	++	+++
1991/1992	A59S/Q289L/S435T	+++	+++	++	+++
1993/1994	Q111K/Q289L/C500L	+++	+++	++	+++

Table 14-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1844)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1844)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
1995/1996	Q111K/Y432L	+++	+++	++	+++
1997/1998	Q289L/S435T/R504A/I556L	+++	+++	++	+++
1999/2000	A59S/Q289L	+++	+++	++	+++
2001/2002	Q111K	+++	+++	++	++
2003/2004	Q289L	+++	+++	++	+++
2005/2006	Q111K/Y432L/C500L	++	++	++	++
2007/2008	Q289L/S435T/C500L/R504A	+++	+++	++	+++
2009/2010	A59S/Y432L/S435T/R504A/I556L	++	++	++	++
2011/2012	A59S/Q66T/Q289L/C500L/R504A/I556L	++	++	++	++
2013/2014	S435T/R504A	++	++	++	++
2015/2016	Q289L/Y432L	++	++	++	++
2017/2018	Q111K/Q289L/S435T/C500L	++	++	++	++
2019/2020	A59S/Q66T/Q111K/Q289L/Y432L/C500L	++	++	++	++
2021/2022	A59S/Q111K/Y432L/C500L	+++	++	++	++
2023/2024	T24K/A59S/Q111K/Q289L/R504A	++	++	++	++
2025/2026	Q66T/Q111K	+++	++	++	++
2027/2028	T24K/Q111K/Q289L	++	++	++	++
2029/2030	Q289L/Y432L/S435T	++	+++	++	++
2031/2032	T24K/Q289L	++	++	++	++
2033/2034	T24K/Q111K/Q289L/C500L/R504A	++	++	++	++
2035/2036	T24K/Q111K/S435T/C500L	+++	++	++	++

Table 14-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1844)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1844)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
2037/2038	R504A/I556L	++	++	++	++
2039/2040	Q111K/A331G/Y432L/R 504A	++	++	++	+++
2041/2042	Q111K/C500L/R504A	+++	++	++	++
2043/2044	Q111K/A331G/S435T/C 500L	++	++	++	++
2045/2046	A59S/Q66T/Q111K/Y43 2L/C500L	+++	++	++	++
2047/2048	A59S/Q66T/Q111K/Y43 2L/R504A	+++	+++	++	++
2049/2050	T24K/Q111K/Y432L	++	++	++	++
2051/2052	A59S/Y432L	++	+++	++	+++
2053/2054	Q111K/Q289L/S435T	++	+++	++	++
2055/2056	R504A	++	+++	++	++
2057/2058	Q289L/S435T	++	+++	++	++
2059/2060	T24K/Y432L/S435T/R50 4A	++	++	++	++
2061/2062	A59S/Q111K	++	+++	++	++
2063/2064	Y432L	++	++	++	++
2065/2066	L211Q/K518S/A519T/T5 47G	+++	++	++	++
2067/2068	Y41Q/L208M/T547G	+++	++	++	++
2069/2070	L208M/L211Q/T547G	++	++	++	++
2071/2072	Y41Q/E51A/M410L/A54 3V	++	++	++	++
2073/2074	E51A/A519T	++	++	++	++
2075/2076	L208M	++	++	++	++
2077/2078	L211Q/T547G	++	++	++	++
2079/2080	L211Q	++	++	++	++
2081/2082	Y41Q/L208M/K518S/A5 19T/T547G	++	++	++	++

Table 14-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 1844) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 1844)	2mM Tyr FIOPC	Protease FIOPC	pH 4 FIOPC	Combined pH and Protease FIOPC
2083/2084	Y41Q/M410L/K518S/T5 47G	++	++	+	++
2085/2086	T547G	++	++	++	++
2087/2088	L208M/L211Q/M410L/A 519T	++	++	++	++
2089/2090	Y41Q/K44P/L208M/T54 7G	++	++	++	++
2091/2092	K44R/L208M/K518S/T5 47G	++	++	++	++
2093/2094	Y41Q/L208M/M410L/A 543V/T547G	++	++	++	++
2095/2096	Y41Q/M410L/K518S/A5 43V	++	++	+	++
2097/2098	A519T	++	++	++	++
2099/2100	M410L	++	++	+	++
2101/2102	Y41Q/A543V	+++	++	++	++
¹ All activities were determined relative to the reference polypeptide of SEQ ID NO: 1844. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; "++" > 1.2; and "+++" > 2.					

EXAMPLE 15

TAL Variants of SEQ ID NO: 2030

[0255] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 2030, for improved tyrosine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 2030, was carried out by constructing libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0256] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4, with the following conditions: 20 μ L of HTP lysate diluted 10-fold in water was assayed with 2.2 mM tyrosine for 5 min. The results of the assays are shown in Table 15-1. Based on the results, SEQ ID NO: 2114 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease and/or Acidic Buffer

[0257] TAL variants were challenged with chymotrypsin and trypsin as described in Example 14. Residual activity was determined as described in Example 10. The results of this assay are shown in Table 15-1.

[0258] TAL variants were challenged with acidic buffer as described in Example 12, with the exception that lysate was incubated with McIlvaine buffer, pH 3.8. Residual activity was determined as described in Example 10. The results of this assay are shown in Table 15-1.

[0259] In some instances, acidic buffer-treated lysate was further challenged with protease in a combined pH and protease assay. Specifically, lysate challenged with acidic buffer as described above was centrifuged, and 50 μ L of the supernatant was incubated with 50 μ L 4 g/L pancreatin dissolved in 100 mM sodium phosphate pH 8. The resulting solution was incubated for 2 h at 37°C, in a THERMOTRON® (INFORS) titre-plate shaker (400 rpm), and residual activity was determined as described in Example 10. The results of this assay are shown in Table 15-1.

Table 15-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 2030) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 2030)	2mM Tyr FIOPC	Protease FIOPC	pH 3.8 FIOPC	Combined pH and Protease FIOPC
2103/2104	A45V/L244M/A324V/K513R	+	++	+	+
2105/2106	A45V/L436I/I512V/K513R	+	++	+	+
2107/2108	K13Q/A45V/I512V	+	++	+	+
2109/2110	K13S/V22T/A45V/I512V	+	++	+	+
2111/2112	K13S/A45V	+	++	+	+
2113/2114	A45V/I512V	+	++	+	+
2115/2116	Q8D	++	++	+	+
2117/2118	L428V	++	++	+	+
2119/2120	T11G	+	++	+	+
2121/2122	A4D	++	++	+	+
2123/2124	A45V	+	++	+	+

Table 15-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 2030) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 2030)	2mM Tyr FIOPC	Protease FIOPC	pH 3.8 FIOPC	Combined pH and Protease FIOPC
2125/2126	T17Q	+	++	+	+
2127/2128	L251V	+	++	+	+
2129/2130	T11D	++	++	+	++
2131/2132	K13R	+	++	+	+
2133/2134	T11A	+	++	+	+
2135/2136	T11S	+	++	+	+
2137/2138	Q8R	++	++	+	+
2139/2140	T11K	+	+	+	+
2141/2142	V341A	+	+	+	+
2143/2144	S19H	+	+	+	+
2145/2146	A324R	+	+	+	+
2147/2148	Q8G	+	+	+	+
2149/2150	I144L		+		+
2151/2152	I327M	+	+	+	+
¹ All activities were determined relative to the reference polypeptide of SEQ ID NO: 2030. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; and "++" > 1.2.					

EXAMPLE 16

TAL Variants of SEQ ID NO: 2114

[0260] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 2114, for improved tyrosine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 2114, was carried out by constructing libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0261] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4, with the following conditions: 20 μ L of HTP lysate diluted 10-fold in water was assayed with 2.2 mM tyrosine

for 5 min. The results of the assays are shown in Table 16-1. Based on the results, SEQ ID NO: 2156 was selected for further directed evolution.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease and/or Acidic Buffer

[0262] TAL variants were challenged with chymotrypsin and trypsin as described in Example 15.

Residual activity was determined as described in Example 10. The results of this assay are shown in Table 16-1.

[0263] TAL variants were challenged with acidic buffer as described in Example 15. Residual activity was determined as described in Example 10. The results of this assay are shown in Table 16-1.

[0264] In some instances, acidic buffer-treated lysate was further challenged with protease in a combined pH and protease assay as described in Example 15, and residual activity was determined as described in Example 10. The results of this assay are shown in Table 16-1.

Table 16-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 2114) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 2114)	2mM Tyr FIOPC	Protease FIOPC	pH 3.8 FIOPC	Combined pH and Protease FIOPC
2153/2154	Q8D/T11D/Q111K/R504A	++	++	++	++
2155/2156	Q8D/T11D/T17Q/V22T/A324V/ R504A/A519T	++	++	++	++
2157/2158	A4D	++	++	++	++
2159/2160	A4D/L428V	++	++	++	++
2161/2162	A4D/Q8R/T11D/K13R/V22T/Q1 11K/R504A	++	++	++	++
2163/2164	A4D/A324V	++	++	++	++
2165/2166	T11D/T17Q/V22T/A324V	++	++	++	++
2167/2168	A4D/Q8D/T11G/T17P/A324V/L 428V/R504A	++	++	++	++
2169/2170	A4D/Q8D/V22T/Q111K/R504A	++	++	++	++
2171/2172	A4D/T17Q/A241S/A519T/T547 A	++	++	+	++
2173/2174	T11G/K13R/R504A	++	++	++	++
2175/2176	Q8D/T11D/K13R/A324V	++	++	++	++
2177/2178	A4D/Q8R/T11D/V22T/Q111K	++	++	++	++

Table 16-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 2114) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 2114)	2mM Tyr FIOPC	Protease FIOPC	pH 3.8 FIOPC	Combined pH and Protease FIOPC
2179/2180	A236V	++	++	+	+
2181/2182	I228M	++	++	+	+
2183/2184	H16Q	++	++	+	++
2185/2186	T437G	++	++	+	++
2187/2188	F10G	++	++	++	++
2189/2190	L316T	+	++		
2191/2192	I2T	++	++	++	++
2193/2194	I228M/Q259H	++	++	+	+
2195/2196	D305E/I307N/I425V	++	++	+	+
2197/2198	V385A	++	++	+	++
2199/2200	T7Q	++	++	+	+
2201/2202	I2G	++	++	+	+
2203/2204	T430E	+	++	+	+
2205/2206	M478L	+	++	+	+
2207/2208	Q6G	++	++	+	+
2209/2210	V57I	++	++	+	+
2211/2212	A39S	++	++	+	+
2213/2214	I425V	++	++	+	+
2215/2216	H16T	++	+	+	+
2217/2218	T505S	+	+	+	+
2219/2220	S14G	++	+	+	+
¹ All activities were determined relative to the reference polypeptide of SEQ ID NO: 2114. Levels of increased activity are defined as follows: ""+"" = 0.9 to 1.2; ""++"" > 1.2; and ""+++"" > 2.					

EXAMPLE 17**TAL Variants of SEQ ID NO: 2156**

[0265] In this Example, experiments for evolution and screening of TAL variants derived from SEQ ID NO: 2156, for improved tyrosine activity, protease resistance, and low pH tolerance are described. Directed evolution of the TAL encoded by SEQ ID NO: 2156, was carried out by constructing

libraries of variant genes. These libraries were then plated, grown, and screened using the methods described below.

HTP Activity Analysis of Clarified Lysates

[0266] HTP growth and lysis of *E. coli* cells expressing TAL variants were performed as described in Example 4. TAL variant activity on tyrosine was assayed as described in Example 4 with the following conditions: 20 μ L of HTP lysate diluted 10-fold in water was assayed with 2.2 mM tyrosine for 5 min. The results of the assays are shown in Table 17-1.

HTP Activity Analysis of Clarified Lysates Pretreated with Protease and/or Acidic Buffer

[0267] TAL variants were challenged with chymotrypsin and trypsin as described in Example 15. Residual activity was determined as described in Example 10. The results of this assay are shown in Table 17-1.

[0268] TAL variants were challenged with acidic buffer as described in Example 15. Residual activity was determined as described in Example 10. The results of this assay are shown in Table 17-1.

[0269] In some instances, acidic buffer-treated lysate was further challenged with protease in a combined pH and protease assay as described in Example 15, and residual activity was determined as described in Example 10. The results of this assay are shown in Table 17-1.

Table 17-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 2156) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 2156)	2mM Tyr FIOPC	Protease FIOPC	pH 3.8 FIOPC	Combined pH and Protease FIOPC
2221/2222	Q111K/M478L	+	+	+	
2223/2224	A241S/V385A/M478L		+		+
2225/2226	H16Q/V57I		+	+	+
2227/2228	V57I/Q111K/P114S	+	+	+	+
2229/2230	T437G	+	+	+	
2231/2232	H16Q/V385A/M478L/T547G		+		+
2233/2234	A241S/V385A/M478L/T547G		+		+
2235/2236	H16Q/V385A/T437G	+	++	+	+
2237/2238	Q111K/A241S/T437G/M478L	+	+	+	+
2239/2240	A241S/V385A	+	++	+	+

Table 17-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 2156) ¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 2156)	2mM Tyr FIOPC	Protease FIOPC	pH 3.8 FIOPC	Combined pH and Protease FIOPC
2241/2242	D20G/V385A/T437G/M478L/ T547G	+	++		+
2243/2244	V57I	+	+	+	+
2245/2246	V385A	+	++	+	+
2247/2248	V385A/T437G/M478L/T547G	+	+		+
2249/2250	H16Q/A241S/T437G	+	++	+	+
2251/2252	H16Q	++	++	+	+
2253/2254	A241S/T437G	+	++	+	+
2255/2256	V57I/T437G	+	+	+	+
2257/2258	H16Q/V385A	+	++	+	+
2259/2260	T437G/M478L	+	+	+	+
2261/2262	A4D/H16Q/V385A/M478L	+	++	+	+
2263/2264	A4D/V57I/Q111K/T437G	++	++	+	+
2265/2266	Q111K/P114S/R202L/Y234H/ L289Q/D305Q/M313L/V324A/ N332K/V336I/M410P/L432Y/ T435S/Q464R/A504R/V512I/T 519A/D523E/K548S/D549G	+	+	+	+
2267/2268	H16Q/Y41Q/T437G	++	+	+	+
2269/2270	F10G/H16Q/T437G	+	+	+	+
2271/2272	A4D/T7Q/V57I/Q111K	++	++	+	++
2273/2274	T7Q/V385A/T547G	+	+	+	+
2275/2276	H16Q/Y41Q/V57I/T437G/M47 8L	+	+		+
2277/2278	M478L	+	+	+	+
2279/2280	A241S	++	+	+	+
2281/2282	H16Q/Y41Q/V57I/Q111K/V38 5A/T547G	+	+		+
2283/2284	H16Q/T437G	+	+	+	+
2285/2286	A4D/T7Q/Q111K/P114S/T437 G/T547G	+	+	+	+

Table 17-1. Relative Activity of TAL Variants on Tyrosine Under Various Conditions (Relative to SEQ ID NO: 2156)¹					
SEQ ID NO: (nt/aa)	Amino Acid Differences (Relative to SEQ ID NO: 2156)	2mM Tyr FIOPC	Protease FIOPC	pH 3.8 FIOPC	Combined pH and Protease FIOPC
2287/2288	V57I/Q111K/M478L/T547G	+	+	+	+
2289/2290	V385A/T437G	+	+	+	+
¹ All activities were determined relative to the reference polypeptide of SEQ ID NO: 2156. Levels of increased activity are defined as follows: "+" = 0.9 to 1.2; and "++" > 1.2.					

[0270] While the invention has been described with reference to the specific embodiments, various changes can be made and equivalents can be substituted to adapt to a particular situation, material, composition of matter, process, process step or steps, thereby achieving benefits of the invention without departing from the scope of what is claimed.

[0271] For all purposes in the United States of America, each and every publication and patent document cited in this disclosure is incorporated herein by reference as if each such publication or document was specifically and individually indicated to be incorporated herein by reference. Citation of publications and patent documents is not intended as an indication that any such document is pertinent prior art, nor does it constitute an admission as to its contents or date.

CLAIMS

WHAT IS CLAIMED IS:

1. A recombinant tyrosine ammonia lyase and/or biologically active recombinant tyrosine ammonia lyase fragment comprising an amino acid sequence comprising at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 2.
2. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution at position or set of positions selected from 79/95/107, 79/107, 79/107/410, 79/410, 95/107/184, 95/107/184/534, 95/184/534, 99/107/184, 107/184/534, and 107/401/534, wherein the positions are numbered with reference to SEQ ID NO: 2.
3. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 28, 29, 33, 33/34/37/46/279/554, 33/34/37/90/554, 33/34/46/66/90/289, 33/34/90/289/554, 33/34/279/289, 33/66, 33/66/289, 33/66/289/554, 34/37/46/289, 34/37/66/279/289, 34/46, 34/56/90, 34/56/90/289, 34/66/289, 34/90/289/554, 34/90/519, 36/70/234/302/461/500, 36/79, 36/79/304/407, 36/79/407/461/500/531, 36/111/304/461/531, 36/407/461/500/531, 37, 46, 46/66/289/519/554, 49, 56, 66, 66/90/279/289/554, 66/90/289/554, 69, 70/79/234/361/407, 70/111/461/500/531, 70/304/407/461, 72, 79/111/234/361/500, 79/111/234/531, 79/111/361, 79/111/531, 79/304/361, 79/304/461/531, 79/407/461, 88, 90/289/519, 90/289/554, 131, 142, 198, 201, 272, 278, 279/289/554, 289/519/554, 289/554, 295, 304/361, 305, 350, 361/500/531, 461/500, 490, 491, 499, 510, 518, 519, 521, 522, 523, 524, 531, 540, 541, 544, 547, 548, 554, 557, 558, and 560, wherein the positions are numbered with reference to SEQ ID NO: 14.
4. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 28/34/49/70/234/289/544/554, 33/34/49/234/531/547/554, 33/34/66/70/519/531, 33/34/66/289/522/531, 33/34/70/234/289/519, 33/34/70/234/518/519/547/554, 33/34/70/289/522/554, 33/34/289/522/531, 34/49/66/531, 34/49/234/531/554, 34/49/289/544/547, 34/66/70/234/518/519/547, 34/66/531/554, 34/66/554, 34/70/234/289/522, 34/70/234/554, 34/70/289/522, 34/234/522/554, 34/289, 34/289/522/531, 34/289/522/544/554, 34/522, 34/544, 66/70/234, and 234/531/544/547, wherein the positions are numbered with reference to SEQ ID NO: 86.

5. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 31, 37/49/56/66/111, 37/49/56/234/557, 37/49/56/500/524, 37/49/66/111/234, 37/49/111/524, 37/111, 37/111/361/500/557/558, 37/234, 43/59/93/506, 43/306, 43/306/506, 49/56/66/111/153/234/500/524, 49/66, 56/111/234, 56/234/500, 61, 65, 65/336, 66, 66/111/234/500, 93/506, 95, 103, 103/107/417/421, 103/306/506, 103/421, 104/105, 107, 107/417/421, 111/234/548/558, 111/361, 145, 146, 155, 172, 197, 211, 234, 234/524, 237/238/506, 286, 304, 306, 306/506, 328, 336, 361/524/557/558, 407, 417/421, 421, 471, 504, 506, 549, and 558, wherein the positions are numbered with reference to SEQ ID NO: 334.

6. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 31/61/95/286/328, 31/61/95/407/504, 31/61/95/471/504, 31/61/407/504, 31/95/155/286/504/549, 31/95/237/504/547/549, 31/95/286/504, 31/95/286/504/549, 31/95/328/504, 31/95/504, 31/95/549, 37/49/56/59/145, 37/103/111/145/421/500/524, 49/56/59/234/500, 49/59/66/111/145/234, 49/59/145/234/421, 56/59/66/234, 56/59/111/145, 56/59/111/145/234/421, 56/66/145/500, 56/103/111/145/234/500, 59/103/145/234/421/500, 59/103/234/421, 59/145, 59/234, 61, 61/95/155/286/407/471, 61/95/155/407, 61/95/286, 61/95/286/328/504, 61/95/328/407, 61/95/328/549, 61/95/407, 61/95/504/547, 61/286/407, 61/328, 61/328/504, 61/328/504/549, 61/407, 61/504, 66/103/145/234/421, 95/155/286/328/407/504, 95/155/286/549, 95/286, 95/286/328/407/504, 95/286/328/504, 95/286/547, 95/287/504/549, 95/328/504, 95/407, 95/407/504, 95/504/547, 95/549, 103/111/145/234/421, 111/145/234, 111/234, 145/234/500, 286/328/407/504/549, and 549, wherein the positions are numbered with reference to SEQ ID NO: 388.

7. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 14/56/114, 14/114/283/289, 14/114/283/289/291, 14/114/283/289/562, 14/114/291/518/562, 14/114/518, 14/234/283/291/305, 14/283/289/562, 29/66/111, 29/66/111/540, 29/111, 29/111/523, 33/46/49, 33/46/49/336/519/548/549, 33/46/49/549, 33/46/518/534/548/549, 33/46/519, 33/49/336, 33/336/519, 36/37/56/59/145/234/328, 36/37/59/131/531, 36/37/103/234, 36/37/131/145/234/328, 36/37/145/234, 36/37/145/234/328/471/531, 36/37/234/328/531, 36/56/145/234/328, 36/59/234/328, 36/59/531, 36/103/145/328/531, 36/131, 36/234/531, 37/56/59/103/145/234/328/471/531, 37/56/59/234/328/524/531, 37/56/59/234/531, 37/56/234/531, 37/59/234, 37/234/471, 46/49, 46/49/518/519/548/549, 46/49/519, 46/155, 46/548, 49/519, 56, 56/59/103/471/531, 56/59/471/531, 56/114/206/283, 56/114/291, 56/114/291/518/562, 56/114/518, 56/518, 59/328/524/531, 66/540, 111, 111/510/521/523/541/558, 111/523/557, 114, 114/206/283/289/562, 114/283/289/291, 114/283/289/305/518, 114/283/291, 114/289, 114/289/562, 114/291, 114/291/518, 114/518/562,

114/562, 131/234/328, 234, 234/328, 234/328/471, 234/531, 289/562, 305, 336/519, 518/519/548/549, 519, 521, 523, 531, 541, 548/549, and 549, wherein the positions are numbered with reference to SEQ ID NO: 604.

8. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 20/49/56/59/111/291, 20/59/234/518/549/562, 49/56/59/66/291/531/549, 49/56/59/111/549, 49/56/66/111/234/291/518, 49/56/66/234, 49/59/66/145/234, 49/59/66/289, 49/59/289/562, 49/66/111/234/291/518/562, 49/111/531, 49/234, 56/59/111/234/289, 56/59/111/234/531, 56/59/111/283/518/531, 56/59/111/291, 56/59/111/291/518/531, 56/59/145/289/518/562, 56/59/234, 56/59/234/518, 56/59/518, 56/111/145/234/289/531/562, 56/111/145/234/518/549/562, 56/111/518/549, 56/234/291, 59, 59/111, 59/145/234/291, 59/234/291, 59/234/291/387/549/562, 111/145, 111/145/234/291/562, 111/145/234/562, 111/234, 111/289, 111/291, 111/518, 234, 234/518/549, 291/518/549, 518, 518/531/549/562, 531, and 549, wherein the positions are numbered with reference to SEQ ID NO: 736.

9. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 33/37, 33/37/46/305, 33/37/103, 33/37/103/305, 33/37/103/305/336/541/548, 33/37/103/305/523/548, 33/37/103/305/548, 33/37/103/336/518/541/548, 33/37/103/471/519/548, 33/37/103/518/523/541, 33/37/103/519/523, 33/37/103/523, 33/37/103/540, 33/37/305, 33/37/305/328, 33/37/305/328/548, 33/37/305/336/471/541, 33/37/305/336/518/523, 33/37/305/336/521/523/548, 33/37/305/336/521/548, 33/37/305/336/541, 33/37/305/471/521/548, 33/37/305/523/540, 33/37/305/540, 33/37/305/541, 33/37/336, 33/37/336/540, 33/37/336/540/548, 33/37/471/523/540/548, 33/37/518/521/540, 33/37/518/521/548, 33/37/518/548, 33/37/521/548, 33/37/523, 33/37/523/540/548, 33/37/540, 33/37/548, 33/46, 33/46/66/305/521/523/540/548, 33/46/103/305/336/518/519/540, 33/46/103/305/336/548, 33/46/103/305/540, 33/46/103/540/548, 33/46/305, 33/46/305/336, 33/46/305/518/540/548, 33/46/336/471/519/523/548, 33/46/336/521, 33/46/336/521/523, 33/46/336/540, 33/46/336/540/548, 33/46/518/521/548, 33/46/521/548, 33/46/523, 33/46/541, 33/46/548, 33/103/336/518/521/548, 33/471/523/541, 37, 37/103, 37/103/305/336, 37/103/305/336/521/523/540/548, 37/103/305/336/523/540, 37/103/305/471, 37/103/305/471/540/548, 37/103/305/521/541/548, 37/103/305/540, 37/103/328/336/518/523/548, 37/103/328/521/541/548, 37/103/336, 37/103/336/521/541, 37/103/519/541/548, 37/103/540, 37/103/541/548, 37/305, 37/305/336, 37/305/336/521/540/548, 37/305/336/523/548, 37/305/336/540/548, 37/305/336/541/548, 37/305/471, 37/305/471/523/540/548, 37/305/471/540/548, 37/305/519/548, 37/305/521/523/540/548, 37/305/521/540, 37/305/521/541/548, 37/305/523/541/548, 37/305/541, 37/305/541/548, 37/305/548, 37/336, 37/336/471/541/548, 37/336/521/523,

37/336/521/523/548, 37/336/523/548, 37/336/540, 37/336/548, 37/471, 37/471/518, 37/471/518/519/523, 37/471/521/540/548, 37/519, 37/521/523/548, 37/521/540, 37/523/541, 37/523/548, 37/540, 37/540/548, 37/541, 37/548, 46, 46/49/59/111/523/531/549, 46/49/111/234/289/436/549, 46/49/111/234/289/531/549, 46/49/111/234/336, 46/49/111/234/336/523/549, 46/49/111/336/549, 46/49/234/289/336, 46/49/234/336/521/523/549, 46/49/234/540/549, 46/49/234/549, 46/49/289/523/531/549/562, 46/49/531/549, 46/59/234, 46/59/549/562, 46/103/305, 46/103/305/336/471/540/548, 46/103/305/336/523, 46/103/305/471/540/548, 46/103/305/520/540, 46/103/305/548, 46/103/523/548, 46/103/540/548, 46/103/541, 46/103/541/548, 46/103/548, 46/111/234/289/531/549, 46/111/234/521/549, 46/111/523/531/549, 46/234/289/549, 46/234/521/523/531/540/549, 46/234/549, 46/289/549, 46/305, 46/305/336, 46/305/336/518, 46/305/336/522, 46/305/336/548, 46/305/471, 46/305/523/548, 46/305/548, 46/336/521/523, 46/336/523/548, 46/336/540, 46/336/540/548, 46/521/523, 46/521/523/540, 46/521/523/549, 46/521/548, 46/523/540, 46/523/541/548, 46/541, 46/541/548, 46/548, 46/549, 49, 49/59/111/234/289/521, 49/59/111/289/523, 49/59/234/289/336, 49/59/234/289/336/523/531/549, 49/59/289/305/336, 49/59/289/336, 49/59/336, 49/59/521/531, 49/111, 49/111/234, 49/111/234/289/336/523/531/549, 49/111/234/289/521/523/531/549/562, 49/111/234/289/523/549, 49/111/234/336/521/523, 49/111/234/336/523/531, 49/111/234/523/531/549, 49/111/234/531, 49/111/234/549, 49/111/289, 49/111/289/336/521/549, 49/111/523/531/549, 49/111/531/549, 49/234, 49/234/289, 49/234/289/336/531/549, 49/234/289/523, 49/234/289/523/531/540, 49/234/289/523/549, 49/234/305/549, 49/234/521, 49/234/549, 49/289/305/336/523, 49/289/336, 49/289/336/521/531, 49/336/521/562, 49/521/531/549/562, 49/521/549, 49/523/549, 49/549, 59, 59/111/234/289/305/336/549, 59/111/234/289/305/549, 59/111/289, 59/111/336, 59/549, 103, 103/336/519/548, 103/521/523/540, 111/234/289, 111/234/289/523, 111/289/336/521, 111/289/336/523/549, 111/336/562, 111/521/523/549, 234, 234/289, 234/289/336/523, 234/289/523/531/549/562, 234/289/523/549, 234/289/531, 234/289/549, 234/336, 234/336/531/562, 234/521/523, 234/521/523/549, 234/523/531, 234/531/549, 234/540, 234/549, 234/562, 289, 289/336/549, 289/521/523, 289/521/523/540, 289/521/523/549, 289/523, 305/336/541/548, 336/548, 519/548, 521, 521/548, 521/549, 521/562, 523, 531/549, 540, and 549, wherein the positions are numbered with reference to SEQ ID NO: 736.

10. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 24/44/464, 24/201/202/351/507, 24/202/351, 33/37/46/56/103/523/540/548/549, 33/37/46/56/111/234/523, 33/37/46/56/111/523/540, 33/37/46/103/111/234, 33/37/46/103/111/548/549, 33/37/46/103/523, 33/37/46/111/234/328/523/540/548, 33/37/46/111/336/540, 33/37/46/234/523, 33/37/46/336, 33/37/46/548/549, 33/37/56/111/234/523/540/548, 33/37/56/234/523/540/548, 33/37/103/111/234/336/540/548,

33/37/103/336/523/540/548, 33/37/111/234/523/540/548, 33/37/111/523/540, 33/37/111/548, 33/37/234/336/523/548, 33/37/523/540/548, 33/46, 33/46/56/111/548, 33/46/56/234/248/549, 33/46/103/523/549, 33/56/103/111, 33/103/111/234, 33/103/111/234/336/523/548, 33/103/111/234/540/549, 33/103/111/336, 33/111/234/548, 33/234/328/523/540/549, 33/234/336/523/540/548/549, 33/234/523/540/548, 33/234/523/548, 33/234/540/548/549, 33/336, 33/336/523/540/548/549, 33/336/540/548, 33/336/549, 37, 37/46/56/523, 37/46/234, 37/46/336/523/540/548, 37/46/336/540/548, 37/56/234/336/523/540/548/549, 37/56/336/523/540/548, 37/103/336/548/549, 37/111/523, 37/234/328/336/523, 37/336, 37/548/549, 44, 46/103/328/336/523, 46/103/336, 46/234/336, 46/234/540/548, 46/336/540/549, 202, 202/332/408, 234/523/540/548/549, 336/523, 408, and 523/548, wherein the positions are numbered with reference to SEQ ID NO: 790.

11. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 74, 102, 210, 313, 391, 392, 402, 415, 417, 418, 420, 424, 506, and 530, wherein the positions are numbered with reference to SEQ ID NO: 790.

12. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 24, 24/44, 24/44/46/202/391, 24/44/111/202/464/506, 24/44/202/313/391/540, 24/44/549, 24/46/102/313/506, 24/46/103/111/464/506/549, 24/46/103/391/506, 24/46/111/313/391, 24/46/111/313/549, 24/46/111/506, 24/46/202/391/506, 24/46/549, 24/103/202, 24/202, 44/46/102/202/313/417, 44/46/103/111/391, 44/46/103/202/313/391, 44/46/103/202/417/464, 44/103/111/313/391/540, 44/111/464/506, 46/103/506, 46/111/417, 46/111/506, 46/202, 46/202/506/549, 46/313/391/540, 103/313/549, 111, 111/202, 111/202/313/391/464, 111/202/313/391/506, 111/202/313/417/540/549, 111/202/391, 111/202/391/540, 111/464/540/549, 202/313/391/549, 202/417/464/540/549, 202/464/506, 202/506/540, 202/506/540/549, 313/391/540/549, and 417, wherein the positions are numbered with reference to SEQ ID NO: 1454.

13. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 20/44/202/506, 20/103/111/471/506, 20/202/313/471/506, 24, 27, 33, 36, 41, 44, 44/111/202/464/471/506/549, 44/202/464/506, 46, 48, 50, 51, 55, 56/111/506, 56/506, 59, 66, 66/528, 103/111/202/464/471, 103/111/471, 103/202/540, 103/464/549, 103/471, 111, 111/202/313/316, 111/202/313/471/506, 111/202/471, 111/506, 197, 202, 202/313/464/471/506, 202/464/506, 202/464/506/549, 208, 272, 289, 292/553, 305, 312/559, 313/464/471/506, 331, 332, 432, 435, 464,

464/506, 470, 500, 504, 506, 506/549, 518, 519, 523, 540, 543, 547, 547/553, 555, 556, and 559, wherein the positions are numbered with reference to SEQ ID NO: 1578.

14. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 20, 20/44/208/272/519, 20/111/208/272/410/432, 20/197/432/519, 24, 24/46/410/435/518, 36/55/305/332/410, 36/66/197/305/332/457, 36/66/197/305/410, 36/66/305, 36/66/305/332/410, 36/66/305/500, 36/197/305, 36/197/305/332/410, 36/197/305/332/410/500, 36/197/305/332/410/559, 36/197/305/332/500, 36/197/305/410, 36/197/305/500, 36/305, 36/305/332, 36/305/332/410, 36/305/410, 41/44/46/111/272, 41/432/526, 44/46/111/208, 44/46/111/432/519, 44/111/432/519/526, 44/208/432/435, 46/111/208/272/435/526, 46/208/272/432/435/526, 46/432/471, 55/305, 55/305/332/457/543/547, 55/305/500/559, 66/305, 66/305/332, 111, 111/272/432/435, 111/272/471/526, 111/272/519, 111/432/435, 111/432/526, 111/526, 134/202/305, 197/305, 197/305/332/410, 197/305/332/500/543/547, 197/305/410, 197/305/500, 208, 208/272/432, 208/410/435, 208/435/519, 211/410, 272, 272/435/526, 298/410, 305, 305/332, 305/332/410, 305/332/410/500, 305/332/457, 305/332/457/500, 305/332/457/555, 305/332/500, 305/410, 305/500/543/547, 410, 432/526, 435, 435/518, 435/519/526, 471, 471/526, and 519, wherein the positions are numbered with reference to SEQ ID NO: 1660.

15. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 24/59/111/289/504, 24/111/289, 24/111/289/500/504, 24/111/432, 24/111/435/500, 24/289, 24/432/435/504, 41/44/208/547, 41/51/410/543, 41/208/410/543/547, 41/208/518/519/547, 41/208/547, 41/410/518/543, 41/410/518/547, 41/543, 44/208/518/547, 51/519, 59/66/111/289/432/500, 59/66/111/432/500, 59/66/111/432/504, 59/66/289/500/504/556, 59/111, 59/111/432/500, 59/289, 59/289/435, 59/432, 59/432/435/504/556, 66/111, 111, 111/289, 111/289/435, 111/289/435/500, 111/289/500, 111/331/432/504, 111/331/435/500, 111/432, 111/432/500, 111/500/504, 208, 208/211/410/519, 208/211/547, 211, 211/518/519/547, 211/547, 289, 289/432, 289/432/435, 289/435, 289/435/500/504, 289/435/504/556, 289/504, 410, 432, 435/504, 504, 504/556, 519, and 547, wherein the positions are numbered with reference to SEQ ID NO: 1844.

16. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 4, 8, 11, 13, 13/22/45/512, 13/45, 13/45/512, 17, 19, 45, 45/244/324/513, 45/436/512/513, 45/512, 144, 251, 324, 327, 341, and 428, wherein the positions are numbered with reference to SEQ ID NO: 2030.

17. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 2, 4, 4/8/11/13/22/111/504, 4/8/11/17/324/428/504, 4/8/11/22/111, 4/8/22/111/504, 4/17/241/519/547, 4/324, 4/428, 6, 7, 8/11/13/324, 8/11/17/22/324/504/519, 8/11/111/504, 10, 11/13/504, 11/17/22/324, 14, 16, 39, 57, 228, 228/259, 236, 305/307/425, 316, 385, 425, 430, 437, 478, and 505, wherein the positions are numbered with reference to SEQ ID NO: 2114.

18. The recombinant tyrosine ammonia lyase of Claim 1, wherein said tyrosine ammonia lyase comprises at least one substitution in at least one position or set of positions selected from 4/7/57/111, 4/7/111/114/437/547, 4/16/385/478, 4/57/111/437, 7/385/547, 10/16/437, 16, 16/41/57/111/385/547, 16/41/57/437/478, 16/41/437, 16/57, 16/241/437, 16/385, 16/385/437, 16/385/478/547, 16/437, 20/385/437/478/547, 57, 57/111/114, 57/111/478/547, 57/437, 111/114/202/234/289/305/313/324/332/336/410/432/435/464/504/512/519/523/548/549, 111/241/437/478, 111/478, 241, 241/385, 241/385/478, 241/385/478/547, 241/437, 385, 385/437, 385/437/478/547, 437, 437/478, and 478, wherein the positions are numbered with reference to SEQ ID NO: 2156.

19. The recombinant tyrosine lyase variant of Claim 1, comprising any variant provided in Tables 1-1, 2-1, 3-1, 4-1, 5-1, 6-1, 7-1, 8-1, 9-1, 9-2, 10-1, 10-2, 11-1, 12-1, 13-1, 14-1, 15-1, 16-1, and 17-1.

20. The recombinant tyrosine lyase variant of any of Claims 1-19, wherein said variant comprises at least about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO: 2.

21. A recombinant tyrosine lyase variant comprising at least 90% sequence identity to at least one of the even numbered sequences in SEQ ID NOS: 10-2290.

22. The recombinant tyrosine lyase variant of Claim 21, wherein the polypeptide of said recombinant tyrosine ammonia lyase comprises one of the even-numbered sequences of SEQ ID NOS: 10-2290.

23. A recombinant tyrosine ammonia lyase comprising a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the polypeptide sequence of SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

24. The recombinant tyrosine ammonia lyase of any of Claims 1-23, wherein said recombinant tyrosine ammonia lyase is thermostable.

25. The recombinant tyrosine ammonia lyase of any of Claims 1-24, wherein said recombinant tyrosine ammonia lyase is resistant to proteolysis.

26. The recombinant tyrosine ammonia lyase of Claim 25, wherein said recombinant tyrosine ammonia lyase is resistant to at least one digestive tract protease.

27. The recombinant tyrosine ammonia lyase of Claim 26, wherein said digestive tract protease is selected from chymotrypsin, trypsin, carboxypeptidases, and elastases.

28. The recombinant tyrosine ammonia lyase of any of Claims 1-27, wherein said recombinant tyrosine ammonia lyase is acid stable.

29. The recombinant tyrosine ammonia lyase of any of Claims 1-28, wherein said recombinant tyrosine ammonia lyase is acid stable and resistant to proteolysis.

30. The recombinant tyrosine ammonia lyase of any of Claims 1-29, wherein said recombinant tyrosine ammonia lyase is purified.

31. The recombinant tyrosine ammonia lyase of any of Claims 1-30, wherein said recombinant tyrosine ammonia lyase exhibits at least one improved property selected from: i) enhanced catalytic activity; ii) reduced sensitivity to proteolysis; iii) increased tolerance to acidic pH; iv) reduced aggregation; v) decreased K_m for tyrosine; vi) decreased immunogenicity; or a combination of any of i), ii), iii), iv), v), and/or vi), as compared to a reference sequence.

32. The recombinant tyrosine ammonia lyase of Claim 31, wherein said reference sequence is selected from SEQ ID NO: 2, 14, 86, 334, 388, 604, 736, 790, 1454, 1578, 1660, 1844, 2030, 2114, and/or 2156.

33. A composition comprising at least one recombinant tyrosine ammonia lyase of any of Claims 1-32.

34. A recombinant polynucleotide sequence encoding at least one recombinant tyrosine ammonia lyase set forth in any of Claims 1-32.

35. The recombinant polynucleotide sequence of Claim 34, wherein said polynucleotide sequence is codon-optimized.

36. The recombinant polynucleotide sequence of Claim 34 and/or 35, wherein said polynucleotide comprises at least 90% sequence identity to at least one of the odd-numbered sequences of SEQ ID NOS: 9-2289.

37. The recombinant polynucleotide sequence of Claim 36, wherein said polynucleotide comprises an odd-numbered sequence of SEQ ID NOS: 9-2289.

38. An expression vector comprising a recombinant polynucleotide sequence encoding at least one recombinant tyrosine ammonia lyase of any of Claims 1-32.

39. The expression vector of Claim 38, wherein said recombinant polynucleotide sequence is operably linked to a control sequence.

40. The expression vector of Claim 39, wherein said control sequence is a promoter.

41. The expression vector of Claim 40, wherein said promoter is a heterologous promoter.

42. A host cell comprising the expression vector of any of Claims 38-41.

43. The host cell of Claim 42, wherein said host cell is prokaryotic.

44. The host cell of Claim 42, wherein said host cell is eukaryotic.

45. A method of producing a recombinant tyrosine ammonia lyase, comprising culturing said host cell of any of Claims 42-44, under conditions that said recombinant tyrosine ammonia lyase encoded by said recombinant polynucleotide is produced.

46. The method of Claim 45, further comprising the step of recovering said recombinant tyrosine ammonia lyase.

47. The method of Claim 45 or 46, further comprising the step of purifying said recombinant tyrosine ammonia lyase.

48. A pharmaceutical composition for the treatment of tyrosinemia, comprising the composition of Claim 33.

49. The pharmaceutical composition of Claim 48, further comprising a pharmaceutically acceptable carrier and/or excipient.

50. The pharmaceutical composition of Claims 48 and/or 49, wherein said composition is suitable for oral administration to a human.

51. The pharmaceutical composition of any of Claims 48-50, wherein said composition is in the form of a pill, tablet, capsule, gelcap, liquid, or emulsion.

52. The pharmaceutical composition of any of Claims 48-51, wherein said composition is coadministered with nitisinone.

53. The pharmaceutical composition of Claim 52, wherein said composition comprises nitisinone.

54. The pharmaceutical composition of Claim 51, wherein said pill, tablet, capsule, or gelcap further comprises an enteric coating.

55. The pharmaceutical composition of any of Claims 48-54, wherein said composition is suitable for parenteral injection into a human.

56. A method for treating and/or preventing the symptoms of tyrosinemia or alkaptonuria in a subject, comprising providing a subject having tyrosinemia or alkaptonuria, and providing the pharmaceutical composition of any of Claims 48-55 to said subject.

57. The method of Claim 56, wherein said symptoms of tyrosinemia or alkaptonuria are ameliorated.

58. The method of Claim 56 and/or 57, wherein said subject is able to eat a diet that is less restricted in its phenylalanine and/or tyrosine content than diets required by subjects exhibiting the symptoms of tyrosinemia or alkaptonuria.

59. The method of any of Claims 56-58, wherein said subject is an infant or child.

60. The method of any of Claims 56-59, wherein said subject is an adult or young adult.

61. A method for the production of L-tyrosine and/or L-tyrosine derivatives comprising the steps of providing at least one recombinant tyrosine ammonia lyase of any of Claims 1-24 and a suitable substrate, and combining said recombinant tyrosine ammonia lyase and said substrate under conditions such that L-tyrosine and/or at least one L-tyrosine derivative is produced.

62. A method for the production of coumaric acid, comprising the steps of providing at least one recombinant tyrosine ammonia lyase of any of Claims 1-32, and a suitable substrate, and combining said recombinant tyrosine ammonia lyase and said substrate under conditions such that coumaric acid is produced.

63. Use of the compositions provided in any of Claims 33, and/or 48-55.

SEQUENCE LISTING

<110> CODEXIS, INC.

<120> ENGINEERED TYROSINE AMMONIA LYASE

<130> CX7-181W02

<140>

<141> 2019-12-06

<150> US 62/779,647

<151> 2018-12-14

<160> 2290

<210> 1

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Wild Type Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc ggttgcgagc ggtgaaccga tttacggcgt taccagcggc 240
ttcgggtggc tggcgaacgt ggttatcacc ccggacctgg cgaaagagct gcagaacaac 300
ctgatgcgtt atcacaaggt ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccggtgc gctggttggt 540
ctgaacgact actataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccc caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gcgagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 2

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Wild Type Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Val	Gly	Ala	Gly	Gln	Lys
		100					105						110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Tyr	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210				215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn


```

gcgggcagcc gtctgattcg tgaggaactg gacggtaccc acgaatatcg tggccaagcg 900
ccgatccagg atcgttacag cctgcgttgc ctggcgcaat atatgggccc gatcgtggac 960
gggtgttgccg aggtggcgca gcaaattgag gttgaaatga acagcgcgac cgacaacccg 1020
ctgattgatg tggagaacca agcgagctac cacggtggca acttcctggg ccagtatatc 1080
ggtatgggca tggaccacct gcgttactat attggcatga tggcgaagca cctggatgtt 1140
caaatcgcgt acctgggtggc gccggagttt aacaacggtc tgccggcgag cctgggtgggt 1200
aacaaggaac gtatcgtgaa catgggcctg aaaggtctgc agatcaccgg taacagcatt 1260
atgccgtgc tgagcttcta cggcaacagc attgcggatc gttacccgac ccacgcggag 1320
caatataacc agaacatcaa cagccaaggt tttgcggcgg cgaacctgac ccgtaacgcg 1380
gttgaaatct tccagcaata tatggcgatt gcgctgatgt ttggtgttca ggcggtggat 1440
ctgcgtacct acgcgtatgc gggtcactat gatgcgagcg agtgcctgag cccgaccacc 1500
cgctgctctgt atcaagcggg gcgtgaagtg gttggtcagc cgccgagcgc ggcgcgtccg 1560
tacatctggg acgatcgtga gcagccgctg gatgaacaca tcgcgaaaat tgcggttgac 1620
atcgcgaccg aaggcgtgat tgttgcggcg gtgaaggacc tgctgaccac cctgaaataa 1680
tga 1683

```

<210> 4

<211> 559

<212> PRT

<213> Artificial Sequence

<220>

<223> Wild Type Tyrosine Ammonia Lyase from *Chroogloeocystis siderophila*

<400> 4

```

Met Asn Thr Val Leu Gln Thr Gln Ala Ser Thr Asn Leu Asn Ala Asp
1           5           10           15
Thr Ile Leu Leu Gly Asp Arg Asn Leu Thr Ile Asp Glu Val Val Ser
          20           25           30
Val Ala Arg His Arg Ala Lys Val Gln Ile Ser Thr Ala Asp Asn Val
          35           40           45
Glu Gln Arg Ile Gln Ala Ser Cys Asp Tyr Ile Ala Glu Ala Val Ala
          50           55           60
Thr Gly Arg Pro Ile Tyr Gly Val Thr Ser Gly Phe Gly Gly Met Ala
65           70           75           80
Asn Val Val Ile Ser Arg Glu Tyr Ala Asp Leu Leu Gln His Asn Leu
          85           90           95
Val Trp Tyr His Lys Val Gly Ala Gly His Lys Leu Pro Leu Thr Asp
          100          105          110
Val Arg Ala Ala Met Leu Leu Arg Val Asn Ser His Leu His Gly Ala
          115          120          125
Ser Gly Ile Arg Arg Glu Ile Val Gln Arg Met Glu Thr Phe Leu Asn
          130          135          140
Ala Arg Val Thr Pro His Val Pro Glu Tyr Gly Ser Ile Gly Ala Ser
145          150          155          160
Gly Asp Leu Thr Pro Leu Ser Tyr Ile Thr Gly Ala Leu Ile Gly Leu
          165          170          175
Asp Glu Arg Tyr Lys Val Asp Phe Asp Gly Glu Glu Ile Asp Ala Ile
          180          185          190
Thr Ala Leu Glu Arg Leu Gly Leu Pro Gln Leu Gln Leu Gln Ala Lys
          195          200          205
Glu Gly Leu Ala Met Met Asn Gly Thr Ser Val Met Thr Gly Ile Ala
210          215          220

```

Ala	Asn	Cys	Val	Tyr	Asp	Thr	Arg	Leu	Leu	Met	Ala	Leu	Thr	Met	Gly	225	230	235	240
Ala	His	Ala	Leu	Ile	Leu	Gln	Gly	Leu	Asn	Gly	Thr	Asn	Gln	Ser	Phe	245	250	255	
His	Pro	Phe	Ile	His	Glu	Leu	Lys	Pro	His	Pro	Gly	Gln	Lys	Trp	Ala	260	265	270	
Ala	Ser	Thr	Met	Leu	Asp	Leu	Leu	Ala	Gly	Ser	Arg	Leu	Ile	Arg	Glu	275	280	285	
Glu	Leu	Asp	Gly	Thr	His	Glu	Tyr	Arg	Gly	Gln	Ala	Pro	Ile	Gln	Asp	290	295	300	
Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Ala	Gln	Tyr	Met	Gly	Pro	Ile	Val	Asp	305	310	315	320
Gly	Val	Ala	Gln	Val	Ala	Gln	Gln	Ile	Glu	Val	Glu	Met	Asn	Ser	Ala	325	330	335	
Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Glu	Asn	Gln	Ala	Ser	Tyr	His	Gly	340	345	350	
Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Met	Gly	Met	Asp	His	Leu	Arg	355	360	365	
Tyr	Tyr	Ile	Gly	Met	Met	Ala	Lys	His	Leu	Asp	Val	Gln	Ile	Ala	Tyr	370	375	380	
Leu	Val	Ala	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	Ala	Ser	Leu	Val	Gly	385	390	395	400
Asn	Lys	Glu	Arg	Ile	Val	Asn	Met	Gly	Leu	Lys	Gly	Leu	Gln	Ile	Thr	405	410	415	
Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Ser	Phe	Tyr	Gly	Asn	Ser	Ile	Ala	420	425	430	
Asp	Arg	Tyr	Pro	Thr	His	Ala	Glu	Gln	Tyr	Asn	Gln	Asn	Ile	Asn	Ser	435	440	445	
Gln	Gly	Phe	Ala	Ala	Ala	Asn	Leu	Thr	Arg	Asn	Ala	Val	Glu	Ile	Phe	450	455	460	
Gln	Gln	Tyr	Met	Ala	Ile	Ala	Leu	Met	Phe	Gly	Val	Gln	Ala	Val	Asp	465	470	475	480
Leu	Arg	Thr	Tyr	Ala	Tyr	Ala	Gly	His	Tyr	Asp	Ala	Ser	Glu	Cys	Leu	485	490	495	
Ser	Pro	Thr	Thr	Arg	Arg	Leu	Tyr	Gln	Ala	Val	Arg	Glu	Val	Val	Gly	500	505	510	
Gln	Pro	Pro	Ser	Ala	Ala	Arg	Pro	Tyr	Ile	Trp	Asp	Asp	Arg	Glu	Gln	515	520	525	
Pro	Leu	Asp	Glu	His	Ile	Ala	Lys	Ile	Ala	Val	Asp	Ile	Ala	Thr	Glu	530	535	540	
Gly	Val	Ile	Val	Ala	Ala	Val	Lys	Asp	Leu	Leu	Thr	Thr	Leu	Lys		545	550	555	

<210> 5

<211> 1524

<212> DNA

<213> Artificial Sequence

<220>

<223> Wild Type Tyrosine Ammonia Lyase from Flavobacterium johnsoniae

<400> 5

atgaacacca tcaacgagta tctgagcctg gaggaattcg aagcgatcat ttttggtaac 60
 caaaaggtga ccattagcga tgtggtttgtg aaccgtgtta acgagagctt caactttctg 120

```

aaggaattca gcggtaacaa agttatctac ggcgtgaaca ccggttttgg cccgatggcg 180
cagtatcgta ttaaagaaag cgaccagatc caactgcagt acaacctgat ccgtagccac 240
agcagcggta ccggtaaacc gctgagcccg gtgtgcgcga aagcggcgat cctggcgcgt 300
ctgaacaccc tgagcctggg taacagcggc gttcacccga gcgtgattaa cctgatgagc 360
gagctgatca acaaggatat taccccgtg atcttcgaac atggtggcgt tgggtgcgagc 420
ggtgacctgg tgcaactgag ccacctggcg ctggttctga tcggcgaggg cgaagtgttc 480
tataagggcg agcgtcgtcc gaccccgga gtgtttgaga ttgaaggcct gaaaccgatt 540
caggttgaga tccgtgaagg tctggcgctg attaacggca ccagcgtgat gaccggtatc 600
ggcgttgatga acgtttatca cgcgaagaaa ctgctggatt ggagcctgaa aagcagctgc 660
gcgatcaacg agctggtgca agcgtacgac gatcacttca gcgcggaact gaaccagacc 720
aagcgtcaca aaggtcaaca agagatcgcg ctgaagatgc gtcagaacct gagcgacagc 780
accctgattc gtaaactgta ggatcacctg tacagcggtg aaaacaccga ggaaatcttc 840
aaggagaagg ttcaagaata ctatagcctg cgttgcgttc cgcagattct gggcccgggtg 900
ctggaaacca ttaacaacgt tgcgagcatc ctggaggacg aattcaacag cgcgaacgac 960
aaccgatca ttgatgttaa gaaccaacac gtgtaccacg gtggcaactt tcacggtgac 1020
tatatcagcc tggagatgga taagctgaaa atcgttatta ccaagctgac catgctggcg 1080
gaacgtcagc tgaactatct gctgaacagc aaaatcaacg agctgctgcc gccgttcgtg 1140
aacctgggta ccctgggctt caactttggt atgcaaggcg ttcagtttac cgcgaccagc 1200
accaccgcgg aaagccaaat gctgagcaac ccgatgtacg tgcacagcat tccgaacaac 1260
aacgacaacc aggatatcgt tagcatgggt accaacagcg cggttattac cagcaagggtg 1320
atcgagaacg cgttcgaagt gctggcgatt gagatgatca ccattgttca agcgatcgac 1380
tatctgggcc agaaggataa aattagcagc gtgagcaaga aatggtacga cgagatccgt 1440
aacatcattc cgaccttcaa agaagatcaa gttatgtacc cgtttgttca gaaggtgaaa 1500
gaccacctga ttaacaacta atga                                     1524

```

<210> 6

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> Wild Type Tyrosine Ammonia Lyase from Flavobacterium johnsoniae

<400> 6

```

Met Asn Thr Ile Asn Glu Tyr Leu Ser Leu Glu Glu Phe Glu Ala Ile
1           5           10          15
Ile Phe Gly Asn Gln Lys Val Thr Ile Ser Asp Val Val Val Asn Arg
          20          25          30
Val Asn Glu Ser Phe Asn Phe Leu Lys Glu Phe Ser Gly Asn Lys Val
          35          40          45
Ile Tyr Gly Val Asn Thr Gly Phe Gly Pro Met Ala Gln Tyr Arg Ile
          50          55          60
Lys Glu Ser Asp Gln Ile Gln Leu Gln Tyr Asn Leu Ile Arg Ser His
65          70          75          80
Ser Ser Gly Thr Gly Lys Pro Leu Ser Pro Val Cys Ala Lys Ala Ala
          85          90          95
Ile Leu Ala Arg Leu Asn Thr Leu Ser Leu Gly Asn Ser Gly Val His
          100         105         110
Pro Ser Val Ile Asn Leu Met Ser Glu Leu Ile Asn Lys Asp Ile Thr
          115         120         125
Pro Leu Ile Phe Glu His Gly Gly Val Gly Ala Ser Gly Asp Leu Val
          130         135         140
Gln Leu Ser His Leu Ala Leu Val Leu Ile Gly Glu Gly Glu Val Phe

```

145					150					155				160
Tyr	Lys	Gly	Glu	Arg	Arg	Pro	Thr	Pro	Glu	Val	Phe	Glu	Ile	Glu
				165					170					175
Leu	Lys	Pro	Ile	Gln	Val	Glu	Ile	Arg	Glu	Gly	Leu	Ala	Leu	Asn
			180					185					190	
Gly	Thr	Ser	Val	Met	Thr	Gly	Ile	Gly	Val	Val	Asn	Val	Tyr	His
		195				200					205			Ala
Lys	Lys	Leu	Leu	Asp	Trp	Ser	Leu	Lys	Ser	Ser	Cys	Ala	Ile	Asn
	210				215					220				Glu
Leu	Val	Gln	Ala	Tyr	Asp	Asp	His	Phe	Ser	Ala	Glu	Leu	Asn	Gln
225				230					235					240
Lys	Arg	His	Lys	Gly	Gln	Gln	Glu	Ile	Ala	Leu	Lys	Met	Arg	Gln
			245						250					255
Leu	Ser	Asp	Ser	Thr	Leu	Ile	Arg	Lys	Arg	Glu	Asp	His	Leu	Tyr
		260					265						270	Ser
Gly	Glu	Asn	Thr	Glu	Glu	Ile	Phe	Lys	Glu	Lys	Val	Gln	Glu	Tyr
	275					280						285		Tyr
Ser	Leu	Arg	Cys	Val	Pro	Gln	Ile	Leu	Gly	Pro	Val	Leu	Glu	Thr
	290				295					300				Ile
Asn	Asn	Val	Ala	Ser	Ile	Leu	Glu	Asp	Glu	Phe	Asn	Ser	Ala	Asn
305				310					315					320
Asn	Pro	Ile	Ile	Asp	Val	Lys	Asn	Gln	His	Val	Tyr	His	Gly	Gly
			325					330					335	Asn
Phe	His	Gly	Asp	Tyr	Ile	Ser	Leu	Glu	Met	Asp	Lys	Leu	Lys	Ile
		340					345					350		Val
Ile	Thr	Lys	Leu	Thr	Met	Leu	Ala	Glu	Arg	Gln	Leu	Asn	Tyr	Leu
	355					360					365			Leu
Asn	Ser	Lys	Ile	Asn	Glu	Leu	Leu	Pro	Pro	Phe	Val	Asn	Leu	Gly
	370			375					380					Thr
Leu	Gly	Phe	Asn	Phe	Gly	Met	Gln	Gly	Val	Gln	Phe	Thr	Ala	Thr
385				390					395					400
Thr	Thr	Ala	Glu	Ser	Gln	Met	Leu	Ser	Asn	Pro	Met	Tyr	Val	His
			405					410					415	Ser
Ile	Pro	Asn	Asn	Asn	Asp	Asn	Gln	Asp	Ile	Val	Ser	Met	Gly	Thr
		420					425					430		Asn
Ser	Ala	Val	Ile	Thr	Ser	Lys	Val	Ile	Glu	Asn	Ala	Phe	Glu	Val
	435					440					445			Leu
Ala	Ile	Glu	Met	Ile	Thr	Ile	Val	Gln	Ala	Ile	Asp	Tyr	Leu	Gly
	450			455					460					Gln
Lys	Asp	Lys	Ile	Ser	Ser	Val	Ser	Lys	Lys	Trp	Tyr	Asp	Glu	Ile
465				470					475					Arg
Asn	Ile	Ile	Pro	Thr	Phe	Lys	Glu	Asp	Gln	Val	Met	Tyr	Pro	Phe
			485				490						495	Val
Gln	Lys	Val	Lys	Asp	His	Leu	Ile	Asn	Asn					
		500					505							

<210> 7

<211> 2085

<212> DNA

<213> Artificial Sequence

<220>

<223> Wild Type Tyrosine Ammonia Lyase from *Rhodotorula glutinis*

<400> 7

```
atggcgccgc gtccgaccag ccagagccag gcgcgtacct gcccgaccac ccaggtgacc 60
caagttgaca tcgtggagaa gatgctggcg gcgccgaccg acagcaccct ggaactggat 120
ggttacagcc tgaacctggg tgatgtggtt agcgcggcgc gtaagggtcg tccggtgctg 180
gttaaagaca gcgatgagat ccgtagcaag attgataaaa gcgttgaatt cctgctgtagc 240
cagctgagca tgagcgttta tgggtgtgacc accggttttg gtggcagcgc ggacacccgt 300
accgaggatg cgatcagcct gcagaaagcg ctgctggaac accaactgtg cgggtgtgctg 360
ccgagcagct tcgatagctt tcgtctgggt cgtggcctgg aaaacagcct gccgctggaa 420
gtggttcgtg gtgcgatgac cattcgtgtt aacagcctga cccgtggtca cagcgcggtg 480
cgtctgggtg ttctggaggc gctgaccaac ttcctgaacc acggcatcac cccgattgtt 540
ccgctgctg gtaccattag cgcgagcggg gatctgagcc cgctgagcta cattgcggcg 600
gcgattagcg gtcacccgga tagcaaggtg cacgtggttc acgaaggcaa ggagaaaatt 660
ctgtatgctg gtgaagcgat ggcgctgttt aacctggagc cgggtggttct ggggtccgaaa 720
gaaggtctgg gcctgggttaa cggtagcgcg gtgagcgcga gcatggcgac cctggcgctg 780
cacgacgcgc acatgctgag cctgctgagc caaagcctga ccgcatgac cgttgaggcg 840
atggtgggtc acgcgggcag cttccaccgc tttctgcacg atgttaccgc tccgcaccgc 900
acccagattg aggtggcggg taacattcgt aagctgctgg aaggcagccg tttcgcggtt 960
caccacgagg aagaggtgaa ggttaaagac gatgaaggta tcctgctgca ggaccgttac 1020
ccgctgctga ccagcccga atggctgggt ccgctgggta gcgatctgat ccatgctgat 1080
gcggtgctga ccattgaggc gggctcagagc accaccgaca acccgctgat cgatgttgaa 1140
aacaagacca gccaccacgg tggcaacttc caagcggcgg cgggtggcgaa caccatggag 1200
aagaccgctc tgggtctggc gcagattggc aaactgaact ttacccaact gaccgagatg 1260
ctgaacgcgg gtatgaaccg tggcctgccg agctgcctgg cggcggaaga cccgagcctg 1320
agctaccact gcaaaggtct ggatattgct gcggcggcgt ataccagcga gctgggtcac 1380
ctggcgaacc cggttaccac ccattgtgcag ccggcggaaa tggcgaacca agcggttaac 1440
agcctggcgc tgattagcgc gcgtcgtacc accgaaagca acgacgttct gagcctgctg 1500
ctggcgaccc acctgtactg cgtgctgcaa gcgatcgatc tgcgtgctgat tgaattcgag 1560
ttaaagaaac agttcgggtc ggcgatcgtg agcctgattg accaactt tggtagcgcg 1620
atgaccggca gcaacctgcg tgatgaactg gttgagaagg tgaacaaaac cctggcgaag 1680
cgtctggagc agaccaacag ctatgacctg gttccgcgtt ggcacgatgc gttcagcttt 1740
gcggcgggca ccgtggttga agtgctgagc agcaccagcc tgagcctggc ggcggttaac 1800
gcgtggaaag ttgcggcggc ggagagcgcg atcagcctga cccgtcaagt gcgtgaaacc 1860
ttctggagcg cggcgagcac cagcagcccg gcgctgagct acctgagccc gcgtacccaa 1920
attctgtatg cgttcgttcg tgaagagctg ggtgtgaagg cgctcgtgg tgacgttttt 1980
ctgggcaaac aggaagtgc catcggtagc aacgtgagca agatctatga agcgattaaa 2040
agcggccgta ttaacaacgt gctgctgaaa atgctggcgt aatga 2085
```

<210> 8

<211> 693

<212> PRT

<213> Artificial Sequence

<220>

<223> Wild Type Tyrosine Ammonia Lyase from *Rhodotorula glutinis*

<400> 8

```
Met Ala Pro Arg Pro Thr Ser Gln Ser Gln Ala Arg Thr Cys Pro Thr
1           5           10           15
Thr Gln Val Thr Gln Val Asp Ile Val Glu Lys Met Leu Ala Ala Pro
          20          25          30
Thr Asp Ser Thr Leu Glu Leu Asp Gly Tyr Ser Leu Asn Leu Gly Asp
          35          40          45
Val Val Ser Ala Ala Arg Lys Gly Arg Pro Val Arg Val Lys Asp Ser
```

	50					55					60				
Asp 65	Glu	Ile	Arg	Ser	Lys 70	Ile	Asp	Lys	Ser	Val 75	Glu	Phe	Leu	Arg	Ser 80
Gln	Leu	Ser	Met	Ser 85	Val	Tyr	Gly	Val	Thr 90	Thr	Gly	Phe	Gly	Gly 95	Ser
Ala	Asp	Thr	Arg 100	Thr	Glu	Asp	Ala	Ile 105	Ser	Leu	Gln	Lys	Ala 110	Leu	Leu
Glu	His	Gln 115	Leu	Cys	Gly	Val	Leu	Pro 120	Ser	Ser	Phe	Asp 125	Ser	Phe	Arg
Leu	Gly 130	Arg	Gly	Leu	Glu	Asn 135	Ser	Leu	Pro	Leu	Glu 140	Val	Val	Arg	Gly
Ala 145	Met	Thr	Ile	Arg	Val 150	Asn	Ser	Leu	Thr	Arg 155	Gly	His	Ser	Ala 160	Val
Arg	Leu	Val	Val	Leu	Glu 165	Ala	Leu	Thr	Asn 170	Phe	Leu	Asn	His	Gly 175	Ile
Thr	Pro	Ile	Val 180	Pro	Leu	Arg	Gly	Thr 185	Ile	Ser	Ala	Ser	Gly 190	Asp	Leu
Ser	Pro	Leu 195	Ser	Tyr	Ile	Ala	Ala 200	Ala	Ile	Ser	Gly	His 205	Pro	Asp	Ser
Lys	Val 210	His	Val	Val	His	Glu 215	Gly	Lys	Glu	Lys	Ile 220	Leu	Tyr	Ala	Arg
Glu 225	Ala	Met	Ala	Leu	Phe 230	Asn	Leu	Glu	Pro	Val 235	Val	Leu	Gly	Pro	Lys 240
Glu	Gly	Leu	Gly	Leu 245	Val	Asn	Gly	Thr	Ala 250	Val	Ser	Ala	Ser	Met 255	Ala
Thr	Leu	Ala	Leu 260	His	Asp	Ala	His	Met 265	Leu	Ser	Leu	Leu	Ser	Gln 270	Ser
Leu	Thr	Ala 275	Met	Thr	Val	Glu	Ala 280	Met	Val	Gly	His	Ala 285	Gly	Ser	Phe
His	Pro 290	Phe	Leu	His	Asp 295	Val	Thr	Arg	Pro	His	Pro 300	Thr	Gln	Ile	Glu
Val 305	Ala	Gly	Asn	Ile	Arg 310	Lys	Leu	Leu	Glu	Gly 315	Ser	Arg	Phe	Ala	Val 320
His	His	Glu	Glu 325	Glu	Val	Lys	Val	Lys	Asp 330	Asp	Glu	Gly	Ile	Leu 335	Arg
Gln	Asp	Arg	Tyr 340	Pro	Leu	Arg	Thr	Ser 345	Pro	Gln	Trp	Leu	Gly 350	Pro	Leu
Val	Ser	Asp 355	Leu	Ile	His	Ala	His 360	Ala	Val	Leu	Thr	Ile 365	Glu	Ala	Gly
Gln	Ser 370	Thr	Thr	Asp	Asn 375	Pro	Leu	Ile	Asp	Val 380	Glu	Asn	Lys	Thr	Ser
His 385	His	Gly	Gly	Asn	Phe 390	Gln	Ala	Ala	Ala 395	Val	Ala	Asn	Thr	Met	Glu 400
Lys	Thr	Arg	Leu 405	Gly	Leu	Ala	Gln	Ile	Gly 410	Lys	Leu	Asn	Phe	Thr 415	Gln
Leu	Thr	Glu	Met 420	Leu	Asn	Ala	Gly	Met 425	Asn	Arg	Gly	Leu	Pro	Ser	Cys
Leu	Ala	Ala 435	Glu	Asp	Pro	Ser	Leu	Ser 440	Tyr	His	Cys	Lys 445	Gly	Leu	Asp
Ile	Ala 450	Ala	Ala	Ala	Tyr	Thr 455	Ser	Glu	Leu	Gly	His 460	Leu	Ala	Asn	Pro
Val 465	Thr	Thr	His	Val	Gln 470	Pro	Ala	Glu	Met	Ala 475	Asn	Gln	Ala	Val	Asn 480
Ser	Leu	Ala	Leu	Ile	Ser	Ala	Arg	Arg	Thr	Thr	Glu	Ser	Asn	Asp	Val


```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 10

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 10

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Lys Glu
      85      90      95
Leu Gln His Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290				295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 11

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 11

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggtgcga ggttgcgct 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt taccacgggt 240
ttcgggtggc tggcgaaagt tggtatcacc ccggacctgg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaaag tgggtcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgact actataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgtg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gcgagcctgg tgggtaacag cgaccgtaaa gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 12

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 12

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ser Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Tyr	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Lys	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
		530				535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 13

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 13

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 14

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 14

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcgaggaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 16
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 16
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Val Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Tyr Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```


Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Lys	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485						490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 17

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 17

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtggtta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgcaagc gggttatcacc ccggacctgg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaaag tgggtgctggc caaaagctga gcctggcgga tgttcgtgctg 360
ggtatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgact attataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctgggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
cctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgcgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagt cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 18
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 18
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ser Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Tyr Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 19

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt taccacgggt 240
ttcggtggca tggcgaacgt tgttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaaag tgggtgcggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgact attataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 20

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 20

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ser	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Tyr	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 21
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 21

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcg	ggt	120
tatggtgcga	aggcgctgct	gaccaccaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	taccacgggt		240
ttcgggtggca	tggcgaaagt	tggtatcacc	ccggacctgg	cgaaagagct	gcagaacaac		300
ctgatgcgtt	atcacaaaag	tggtgcgggc	caaaagctga	gcctggcgga	tggtcgtgcg		360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgctttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg		540
ctgaacgact	actataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
ctgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgaccacag	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc		1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg		1560
agcgaggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	cgatatacac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 22
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 22

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ser	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Tyr	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 23

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 23

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt taccagcggc 240
ttcgggtggc tggcgaaagt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagt ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggc 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```



```

gcgagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagt cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 24

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 24

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Val Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395				400			
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405				410						415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490							495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515				520							525					
Asn	Asp	Asn	Glu	Gln	Ser	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 25

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 25

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgct 120
tatggtgcga aggcgtgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggttatcacc ccggacctgg cgaaagagct gcagaacaac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg cagggtgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggtttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gctgtagacc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagt cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 26

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 26

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ser	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 27
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 27
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt tgttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaaag tgggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaaca tcaccgggtgc gctgggttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagt cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 28
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 28
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ser	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ser	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 29

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 29

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcgacg	aagtggcgag	tggtgcgcg	120
tatgggtgca	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgagggc	gggtgagcgc	ggatgaaccga	tttacggcgt	tacctcgggt	240
ttcggtggca	tggcgaacgt	gggtatcagt	ccggacctgg	cgcgagagct	gcagaataac	300
ctgatgcgtt	atcacaagc	gggtgagggc	caaaagctga	gcctggcgga	tggtcgtgcg	360
ggatgctgc	tgctgagaa	cagccacctg	caggtgagca	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccgggtg	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggatccgcgg	tgatgaccgg	tattgagggc	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgagca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa	840
atgctggagc	tgctggcggg	cagcgccctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgcttgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
ctgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaac	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgcttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcgaggaa	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	cggatatcac	cagcggtggc	cgtattgttc	aagcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 30
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 30
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asp Glu Val Ala Ser Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Ser Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgttc aagcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 32

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 32

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 33

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 33

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgaca aagtggcgca agttgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaacgc gggtgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggtatcact ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtagc cgtattgttc aagcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 34

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 34

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asp Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50           55           60
Ala Asn Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185				190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
			275				280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 35
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 35
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaaag aagtggcgca agttgcgcgt 120
 tatgggtgcga aggcgcgtct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
 ttcggtggca tggcgaacgt gggtatcact ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagcgccctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacag cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aagcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 36
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 36

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ile														

<210> 37

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 37

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgaca aagtggcgca agttgcgcg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaagt taatagcagc 180
tgcgagtggg tggcgaacgc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcggatggc tggcgaacgt gggtatcact ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgct tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacggttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatga tcaccgggtg gctgggttgt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagatt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```



```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aagcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 38
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 38
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asp Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Asn Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Ser Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Glu Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Ala				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 39

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 39

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgacg aagtggcgca agttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcagt ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgttc aagcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 40

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 40

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asp Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Ser Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 41

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 41

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgaca aagtggcgca agttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaacgc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcact ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta taccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgccctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 42

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 42

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asp Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

50	55	60													
Ala	Asn	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 44

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Ser	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370					375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 45

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 45

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaag aagtggcgca agttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagggggg taatagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcagt ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020

```

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cgatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 46

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 46

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Ser Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505					510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 47

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 47

atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg accatcaaga aagtggtgcga agttgcgcgt 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaacgc gggtgagcgg ggtgaaccga ttacaggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcagt ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggatgctgct tgcgtgcaaa cagccacctg cagcgtgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatctggag cgcggatcaa 840
atgctgggag tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgttc aagcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 48

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 48

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Asn Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Ser Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Asp	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
		530				535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 49

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 49

```
atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggtatcagt ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgta caaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgttc aagcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 50

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 50

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Ser	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcgaggaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 52
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 52
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Asn Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455				460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535				540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ile														

<210> 53

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 53

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgacg aagtggcgag tgttgcgctg 120
tatgggtgca aggcgcgtct gaccacaaa gaggaagtgc tgcagaagg taaacagcagc 180
tgcgagtggg tggcgaggc gggtgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcact ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgaggc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgacccg ctggcgatca tcaccgggtg gctgggtggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgcgg ttgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgacga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgagtcaa 840
atgctgggagc tgctggcgggg cagcgccctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcggtggc cgtattgttc aagcgatcaa ccaagtgggt 1680
agcatt

```

<210> 54
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 54
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asp Glu Val Ala Ser Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 55

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgacg aagtggcgca ggttgcgcggt 120
tatggtgcga aggcgcgtct gaccaccaa gaggaagtgc tgcagaaagt taatagcagc 180
tgcgagtggg tggcgaacgc gggtgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcggtaggca tggcgaacgt gggtatcagt ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgctcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcggtggc cgtattgtta aagcgatcaa ccaagtgggt 1680
agcatt
```

<210> 56

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 56

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asp Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Asn Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Ser	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 57
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 57

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaa	ag	aagtggcgcg	tggtgcgcgt	120
tatggtgcga	aggcgcgtct	gaccaccaa	gaggaagtgc	tg	cagaaggt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgagc	ggtgaaccga	tt	tacggcgt	tacctcgggt	240
ttcggtggca	tggcgaacgt	ggttatcact	ccggacctgg	cg	gcggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gc	cctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gc	ggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cg	cacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tc	cacgggtgc	gctgggttgg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tg	accgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aa	ggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	at	gatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tg	aacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aa	atctggag	cgcgagcaa	840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	ag	ctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gt	tcctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tc	gagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gc	taccacgg	tggcaacttc	1080
ctgggccagt	atattggtac	cagcatggac	cgtctgcgtt	ac	tatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	ag	tttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gc	cctgaagg	tctgcagatt	1260
accggtaaca	gcacatgcc	gctgctgacc	ttctacggca	ac	agcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	taacaaaaac	atcaacagcc	ag	gggttttg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cg	atcgcgct	gatgtttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	ac	tacgatgc	gagccaatgc	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aa	gtggttgg	taaagcgccg	1560
agcgaggaac	gtccgtatat	ctggaacgac	aacgagcagg	cg	ctggatga	acacattgcg	1620
ctgatcgcg	cgatatacac	cagcggtggc	cgtattgtta	aa	gcgatcaa	ccaagtgggt	1680
agcatt							1686

<210> 58
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 58

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Arg	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 59

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 59

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgacg aagtggcgca agttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaaagt gggttatcact ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgctgtcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgagtcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aagcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 60

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 60

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asp Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Ser	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280				285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390					395						400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405				410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420					425						430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
		500				505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530				535						540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	
545				550					555						560	
Ser	Ile															

<210> 61

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 61

```

atgatcattg cgagccagac ccaaaccttc accagcaaatt tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaag aagtggcgca agttgcgcgt 120
tatggtgcga aggcgtgctg gaccacaaa gaggaagtgc tgcaggggggt taatagcagc 180
tgcgagtggg tggcgaggc ggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacct ggttatcagt ccggacctgg cggcggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgccctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaacgc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cgatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 62

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 62

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Ser Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 63
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 63
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaag aagtggcgag tgttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaagt taatagcagc 180
tgcgagtggg tggcgaacgc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggttatcact ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgatga tcaccgggtg gctgggtggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgagtcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aagcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 64
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 64
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Ser	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Asn	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Ser	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355						360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 65

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 65

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgctg	120
tatgggtgca	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcgggt	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctga	gcctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatctggag	cgcgagtcaa	840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
ctggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcgaggaa	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	cggatatcac	cagcggtggc	cgtattgttc	aagcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 66
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 66
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Ser Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaaccgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 68

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 68

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Ser Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 69

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 69

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaag aagtggcgca agttgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggtatcagt ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgccctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaaccgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 70

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 70

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Ser Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
			275				280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg</

530		535		540
Asp Ile Thr Ser Gly	Gly Arg Ile Val Lys Ala	Ile Asn Gln Val Val		
545	550	555	560	
Ser Ile				

<210> 71
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 71
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgct 120
 tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgaacgc gggttgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
 ttcgggtggca tggcgaacgt gggttatcagt ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggg 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg cggatatcac cagcgtgggc cgtattgttc aagcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 72
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 72

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Asn	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Ser	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 73

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 73

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggttatcacc cggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggtttttg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaaccgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgttc aagcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 74

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 74

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Ser Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Pro Pro Ser Glu Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Ala				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 75

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 75

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatgggtgca aggcgcgtct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaacgc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcact ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttt atgatgacgca gaacctgctg 720
gcgctgagcc tgggtgacga tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaaccgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgttc aagcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 76

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 76

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Asn Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245				250						255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 77

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 77

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagtgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgaatgacgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg ggcagccgat ccaagatcgt tactcgtcgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cgatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 78

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 78

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

	50					55					60				
Ala 65	Gln	Ala	Val	Ala	Ser 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Leu	Ala	Ala 95	Glu
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg 125	Ala	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser 185	Tyr	Thr	Val	Asp	Phe	Asn 190	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Ala 285	Gly	Ser
Ala 290	Leu	Ile	Arg	Asp	Glu 295	Leu	Asp	Gly	Ser	His 300	Asp	Tyr	Arg	Gly	Gly
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ser	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu 335	Ile
Glu	Ile	Asn 340	Ser	Val	Thr	Asp	Asn 345	Pro	Leu	Ile	Asp	Val	Ala 350	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly 405	Asn	Ser	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr 430	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala 445	Glu	Gln	Phe	Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 80

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 81

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 81

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgct 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tactcgtgct gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020

```

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
atgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 82

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 82

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290				295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Met	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 83

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 83

atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg accatcaaga aagtggtccca ggttgcgct 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg agcagccgat ccaagatcgt tactcgctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacg 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 84

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 84

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 85

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 85

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtg tgcagaagg taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgaaa ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgta caaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccagaata attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcg cggtatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 86

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 86

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280						285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcgaggaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 88
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 88
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Gly
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 89

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 89

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggccca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaaagt gggtatcacc ccggacctgg cggcgagcgt gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcgaa cagccacctg cacgggtgcga gcgggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgcgg ttgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgacga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctgggagc tgctggcgggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg ggcagccgat ccaagatcgt tactcgtgcg gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaactc ggaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
atgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgagggaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 90

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 90

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 91

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgaaa ggtgaaccga ttacggcgtg taccagtggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg ggcagccgat ccaagatcgt tactcgtctg gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
atgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 92

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 92

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Gly	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325						330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Met	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485						490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 93
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 93

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcca	ggttgcgctg	120	
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tcagaaggt	taacagcagc	180	
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	taccactggg	240	
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300	
ctgatgcgtt	atcacaaagc	gggtgcgggc	aaaaagctga	gcctggcgga	tgcttcgtgcg	360	
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420	
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgtttg	cgaatttggg	480	
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg	540	
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600	
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660	
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720	
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780	
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa	840	
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac	900	
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960	
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020	
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080	
ctgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140	
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200	
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260	
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320	
ccgaccacag	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380	
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440	
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500	
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560	
agcgaggaac	gtccgtatat	ctggaacgac	gatgagcagg	cgctggatga	acacattgcg	1620	
ctgatcgcgg	cggatatcac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt	1680	
agcatt						1686	

<210> 94
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 94

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 95

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 95

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtgggtcca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt taccagtggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tactcgctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
atgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacg 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 96
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 96
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Val Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325					330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Met	Thr	Arg	Arg
	450				455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470					475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550					555					560	
Ser	Ile														

<210> 97

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 97

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtgggtcca ggttgcgctg 120
tatggtgcga aggcgtgctg gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt taccagtggg 240
ttcgggtggc tggcgaaagt gggttatcacc ccggacctgg cggcggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc aaaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg ggcagccgat ccaagatcgt tactcgtgct gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
atgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 98

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 98

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Val Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Gly
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Met	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 99
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 99
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt taccagtggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg agcagccgat ccaagatcgt tactcgctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaactc ggaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
atgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacg 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 100
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 100
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355						360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Met	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 101

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 101

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtggtta	ttgtgggtga	taagccgctg	accatcaaga	aagtggccca	ggttgcgctg	120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaaa	ggtgaaccga	tttacggcgt	taccagtggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aaaaagctga	gcctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa	840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	agcagccgat	ccaagatcgt	tactcgctgc	gttgcttgcg	gcagtatacc	960
ggcccattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
ctgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaac	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
atgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaaacg	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg	1560
agcgaggaa	gtccgtatat	ctggaacgac	gatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	cggatatcac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 102
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 102
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tactcgtcgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaacaa 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 104

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 104

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Gln	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 105

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 105

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtgggtcca gggttgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcggg tggttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgacccc ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgac agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
atgaccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacg 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 106

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 106

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Lys Lys Val Val Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
			275					280					285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Met	Thr	Arg	Arg

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 107
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 107
 atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtgggtcca gggtgcgcgt 120
 tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgcaagc gggtgcgaaa ggtgaaccga ttacggcgt taccagtggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcggg tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcagg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
 tacatgggag agcagccgat ccaagatcgt tactcgtgct gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 atgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacg 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
 agcgaggaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg cggatatcac cagcgtgggc cgtattgtta aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 108
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 108

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Val	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Met	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Met	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 109

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 109

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtgggtcca gggtgcgcggt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc cggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tactcgtgct gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 110

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 110

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Val Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Ser Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Glu Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Ala				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 111

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 111

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg accatcaaga aagtgggtcca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg ggcagccgat ccaagatcgt tactcgtgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 112

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 112

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Val Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Gly	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 113

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 113

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgct 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtg tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta taccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 114

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 114

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

50		55		60											
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210					215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					450		455				460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<210> 115
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

$\langle 210 \rangle$ 116

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 116

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370					375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 117

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 117

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgctgagc	ggtgaaccga	tttacggcgt	tacctcgggt		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tggtcgtgctg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtagcgcg	tgatgaccgg	tattgctggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatctggag	cgcgagcagaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac caggggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 118

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 118

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Arg	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 119

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 119

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg accatcaaga aagtggtgcga ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggttatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaat tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 120

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 120

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 121

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 121

```
atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga tgggccgctg accatcaaga aagtggcgca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgacctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcg cggtatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 122

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 122

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Gly	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaggaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 124
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 124
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 125

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 125

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgcg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgcaagc gggttatcacc ccggacctgg cggcgagcgt gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcaag cagccacctg cacgggtgca gcgggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg ttgtagcgagg tattgtagcgagg aactgtagttt atgtagcgca gaacctgtagt 720
gtagctgagcc tgggtgtagca tgcgctggcg ctgtagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctgggagc tgctggcgagg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgc 1500
ctgagcccg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgcc 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattagg 1620
ctgtagcgcg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgg 1680
agcatt

```

<210> 126

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 126

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 127

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcggtaggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgctcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg gggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 128

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 128

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325						330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485						490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Gly
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 129
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 129

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcg	ggttgcgcg	120
tatggtgcga	aggcgctgct	gaccaccaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcgggt		240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgcttcgtgcg		360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg		540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcgggc	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccacccgt	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
ctgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgacccacg	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc		1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg		1560
agcgaggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	cggtatcttc	gagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 130
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 130

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Ser	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 131

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 131

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaaagt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa cgcggtggtt 1680
agcatt
1686

```

<210> 132

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 132

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280				285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Ala	Val	Val	
545				550					555						560	
Ser	Ile															

<210> 133

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 133

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgtgctg gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgtg tacctcgggt 240
ttcgggtggc tggcgaaagt gggttatcacc ccggacctgg cggcggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgt ctgatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 134

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 134

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ser
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 135
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 135
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag cggcgtgacc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcgaggaat atccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 136
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 136
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Tyr	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 137

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 137

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcgt	120
tatgggtgca	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcgggt	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctga	gcctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa	840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agcaggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
ctgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcgagggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	cggatatcac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 138
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 138
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Ala Leu Ile Arg Asp Glu Gln Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatctg tagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 140

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 140

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540	
Asp	Ile	Cys	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 141

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 141

```
atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtagacc cgacgcttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg ttagtaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgctg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
gctatcgctg cggtatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 142

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 142

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

100						105						110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					4				

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 143
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 143
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
 tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
 ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacag cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgt 1440
 gtgcaaagcg ttgacctgcg taccaagaaa gtggcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg cggatatcac cagcgtgggc cgtattgtta aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 144
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 144

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Val	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555							560
Ser	Ile														

<210> 145

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 145

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgggtgaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 146

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 146

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Ser Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Gly Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Ala				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 147

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 147

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgctcggc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcgga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 148

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 148

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Ser Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245				250						255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 149

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 149

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc ggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagtgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg ttagtaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg cggatatcac ccagggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 150

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 150

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```


50		55		60											
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210					215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					450		455				460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 152

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355						360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Glu	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 153

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 153

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taaggagctg	accatcaaga	aagtggcgca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgctgagc	ggtgaaccga	tttacggcgt	tacctcgggt		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cgatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 154

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 154

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Glu Leu Thr Ile
20     25     30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290				295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475						480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 155

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 155

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggtgcga ggttgcgct 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgct ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgacctcg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgagga aaaccgccc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgagg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgacctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaggggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 156

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 156

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Arg	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 157

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 157

```
atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcca gagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 158

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 158

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cacgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 160
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 160
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455				460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535				540					
Asp	Ile	Thr	Thr	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ile														

<210> 161

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 161

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgcg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgcaagc gggttatcacc ccggacctgg cggcgagcgt gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcaag cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctgggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgcgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagatt attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 162

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 162

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 163

```
atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcg 120
tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcggt tacctcgggt 240
ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttgg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg tgttgcccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 164

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 164

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
```


Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325						330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485						490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Val	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 165
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 165

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcg	ggttgcgcg	120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcggt		240
ttcgggtggca	tggcgaaagt	gcagatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgcttcgtgcg		360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgctttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg		540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
ctgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgacccacg	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc		1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg		1560
agcgaggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	cgatatacac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 166
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 166

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Gln	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 167

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 167

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgttgaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 168

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 168

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475						480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Val	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520							525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530					535					540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ile																

<210> 169

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 169

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgct 120
tatggtgcga aggcgtgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggttatcacc ccggacctgg cggcggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgca gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
cggctgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 170

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 170

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Arg	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 171
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 171
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgag tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta gtgcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 172
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 172
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355						360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Ser	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 173

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 173

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taatccgctg	accatcaaga	aagtggcgca	ggttgcgctg	120
tatgggtgca	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcgggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcaaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcaaa	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtgc	aaatctggag	cgcgagcaaa	840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
ctgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgcttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcgagggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	cggatatcac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 174
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 174
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Asn Pro Leu Thr Ile
 20 25 30
 Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 176

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 176

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Cys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 177

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 177

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga ttacggcgct tacctcgggt 240
ttcgggtggc tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtg 360
ggatatgctg tgcgtgcaaa cagccacctg caggtgcaaa gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtc caaccagagc 780
ttccacctgt ttattacca gtgcaaaccc caccgggtc aaatctggag ctcgcagcaa 840
atgctggagc tgctggcgcc cagcgcgctg attcgtgac agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattg 1620
ctgatcgcg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgg 1680
agcatt 1686
```

<210> 178

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 178

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```


			100					105				110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135				140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185				190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265					270			
Gly	Gln	Ile	Trp	Ser	Ser	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345				350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530		535		540
Asp Ile Thr Ser Gly	Gly Arg Ile Val Lys Ala	Ile Asn Gln Val Val		
545	550	555	560	
Ser Ile				

<210> 179
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 179
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
 tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
 ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggg 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa cttgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg cggatatcac cagcgtgggc cgtattgtta aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 180
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 180

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390							395				400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Leu	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 181

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 181

```

atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaata aagtggcgca gggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcggtggca tggcgaacgt gggttatcacc cggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggtttttg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 182

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 182

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Ser Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Glu Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Ala				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 183

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 183

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagaggctg accatcaaga aagtggcgca ggttgcgcg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga ttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 184

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 184

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Arg Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 185

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 185

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggttatcacc ccggaccttg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgag 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 186

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 186

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

50		55		60											
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210					215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					450		455				460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<210> 187
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<210> 188

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 188

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355						360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Gln	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 189

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 189

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020

```

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcgc gagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 190

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 190

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290				295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Ala	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 191

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 191

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggtgcga ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaaagt gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg atgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgtg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 192

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 192

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```


His	Leu	Met	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 193

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 193

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgta ca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac caagggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 194

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 194

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280						285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295						300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375						380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390						395				400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		

agctatgaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
 agcatt 1686

<210> 196
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 196
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Tyr	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 197

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 197

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaggcgctg accatcaaga aagtggcgca gggtgcgct 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgcaagc gggttatcacc ccggacctgg cggcgagcgc gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg ttgtagcgagg tattgtagcgagg aactgtagttt atgtagcgca gaacctgtagt 720
gtagctgagcc tgggtgtagca tgcgctggcg ctgtagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcgagg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgc 1500
ctgagcccg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgcc 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgc 1620
ctgtagcgcg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgg 1680
agcatt 1686

```

<210> 198

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 198

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Ala Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 199

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcggt 120
tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcggtaggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgctcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcggtggc cgtattgttt atgcgatcaa ccaagtgggt 1680
agcatt
```

<210> 200

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 200

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325						330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485						490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Tyr	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 201
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 201

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcg	ggttgcgcg	120
tatggtgcga	aggcgctgct	gaccaccaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcgggt		240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgcttcgtgcg		360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttggt		540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcgggc	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
ctgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgacccacg	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc		1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg		1560
agcgaggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	cgatatacac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgcgg		1680
agcatt							1686

<210> 202
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 202

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Arg
545					550				555						560
Ser	Ile														

<210> 203

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 203

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaaggct attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgct 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 204

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 204

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350
 Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Ile Gly Thr Ser
 355 360 365
 Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp
 370 375 380
 Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro
 385 390 395 400
 Ala Ser Leu Val Gly Asn Ser Asp Arg Pro Val Asn Met Gly Leu Lys
 405 410 415
 Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr
 420 425 430
 Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn
 435 440 445
 Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg
 450 455 460
 Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly
 465 470 475 480
 Val Gln Ser Val Asp Leu Arg Thr Lys Ala Ile Ala Asn His Tyr Asp
 485 490 495
 Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile
 500 505 510
 Lys Glu Val Val Gly Lys Ala Pro Ser Glu Glu Arg Pro Tyr Ile Trp
 515 520 525
 Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Ala
 530 535 540
 Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ile

<210> 205

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 205

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
 tatggtgcga aggcgtgct gaccaataaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
 ttcggtggca tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 206

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 206

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```


145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 207
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 207
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga tgcgccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag cggcgtgacc cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 208
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 208
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Ala Pro Leu Thr Ile
20 25 30

Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 209

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 209

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgctg	120
tatgggtgca	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcgggt	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctga	gcctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcaaa	cagccacctg	cacgggtgca	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgag	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcgggc	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcaaa	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccc	caccggggtc	aaatctggag	cgcgagcaaa	840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgcttgcg	gcagtatacc	960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
ctggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgcttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcgagggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	cggatatcaa	gagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 210
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 210
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaacagccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 212

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 212

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Gln	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 213

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 213

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcg 120
tatgggtgcga aggcgcggct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 214

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 214

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

100						105						110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					4				

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 215
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 215
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgct 120
 tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
 ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttgggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgggt 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcgaggaag ctccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
 ctgatcgcgg cggatatcac cagcgttggc cgtattgtta aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 216
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 216

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Ala	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555							560
Ser	Ile														

<210> 217

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 217

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatggtgcca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcggatggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg caggtgcgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggtttttg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccatgtggtt 1680
agcatt 1686

```

<210> 218

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 218

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Ser Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Glu Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Ala				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn His Val Val				
545		550		555
Ser Ile				560

<210> 219

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 219

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaa ctccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 220

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 220

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```


Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Thr	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 221

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 221

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgct 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgctgct gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacct gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 222

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 222

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

50		55		60											
Ala	Arg	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210					215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					450		455				460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 224

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Glu	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 225

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 225

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcggc	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgctgagc	ggtgaaccga	tttacggcgt	tacctcgggt		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcggga	tggtcgtgctg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatctggag	cgcgagcaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cgatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 226

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 226

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290				295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 227

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 227

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggtgcga ggttgcgct 120


```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgtg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cgctggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 228

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 228

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
						535					540				
Asp	Ile	Thr	Ala	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 229

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 229

```
atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgact 1680
agcatt 1686
```

<210> 230

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 230

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 232
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 232
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100      105      110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115      120      125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130      135      140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145      150      155      160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165      170      175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180      185      190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195      200      205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210      215      220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225      230      235      240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245      250      255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Ser
      260      265      270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275      280      285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290      295      300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305      310      315      320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 233

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 233

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgcg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgcaagc gggttatcacc ccggacctgg cggcgagcgt gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcaag cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg ttgtagcgagg tattgtagcgagg aactgtagttt atgtagcgca gaacctgtagt 720
gtagctgagcc tgggtgtagca tgcgctggcg ctgtagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgtagcaa 840
atgctggagc tgctggcgagg cagcgtagctg attcgtgagc agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgtagc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgtagaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgtagc gatgtttggg 1440
gtgcaaagcg ttgacctgag taccaagaaa attgtagaac actacgatgc gagccaatgc 1500
ctgagcccg ctagcctgca actgtatctg gcgattaagg aagtggtagg taaattgtag 1560
agcaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgag 1620
ctgtagcgag cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 234
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 234
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 235

```
atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcggt 120
tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcggt tacctcgggt 240
ttcggtaggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgcttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaattttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttggg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaaggtg attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 236

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 236

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Val	Ile	Ala	Asn	His	Tyr	Asp	
			485						490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 237
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 237

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcg	ggttgcgcg	120
tatggtgcga	aggcgctgct	gaccaccaa	gaggaagtgc	tcagaaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcgggt		240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgcttcgtgcg		360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgctttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg		540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcgggc	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccacccgt	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
ctgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgacccacg	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc		1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg		1560
agcgaggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	cgatatacac	cagcggtggc	cgtattgttc	gtgcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 238
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 238

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Arg	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 239

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 239

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtataag gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 240

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 240

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Lys	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520							525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530					535					540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ile																

<210> 241

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 241

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgtgctg gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaaagt gggttatcacc ccggacctgg cggcggagct gcagaataac 300

```



```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg cagggtgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcgg tagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 242

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 242

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
				530					535					540	
Asp	Ile	Gly	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 243
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 243
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag cggcgtgacc cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cgggggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 244
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 244
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355						360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Gly	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 245

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 245

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgctg	120
tatgggtgca	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcgggt	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctga	gcctggcgga	tgttcgtgctg	360
ggtatgctgc	tgcgtgcaaa	cagccacctg	cacgggtgca	gcggatatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttgggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctggttgggt	540
ctgaacgaca	gttataacct	tgatttttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcaaa	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa	840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
ctgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaac	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcgaggaat	tgccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcg	cggatatcac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 246
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 246
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggtttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ctcggtggtt 1680
agcatt 1686

```

<210> 248

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 248

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```


Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Ser	Val	Val	545	550	555	560
Ser	Ile																		

<210> 249

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 249

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga ttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggtatgctgc tgcgtgcaaa cagccacctg caggtgcaaa gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtc caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccc caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgctg cggtatcccg gagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 250

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 250

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

100						105						110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					4				

530		535		540
Asp Ile Arg Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 251
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 251
 atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttcgcgt 120
 tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgcaagc gggttcgcagc ggtgaaccga ttacggcgt tacctcgggt 240
 ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgt 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg cggatatcac cagcgtgggc cgtattgtta aggcgatcga gcaagtgggt 1680
 agcatt 1686

<210> 252
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 252

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Glu	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 253

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 253

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
tatgggtgca aggcgctgct gaccgataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataaccg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggtttttg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 254

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 254

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Ser Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Glu Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Ala				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 255

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 255

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgctgagc ggtactccga ttacggcgtg tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc cggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgctggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```



```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 256

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 256

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Thr Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 257

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 257

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccttg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa cgatgtggtt 1680
agcatt
```

<210> 258

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 258

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

50		55		60											
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					450		455				460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp


```
<211> 562
<212> PRT
<213> Artificial Sequence
```

 $\langle 220 \rangle$

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 260

Met 1	Ile	Ile	Ala	Ser 5	Gln	Thr	Gln	Thr	Phe 10	Thr	Ser	Lys	Phe	Pro 15	His
Thr	Ala	Ser	Asp 20	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu 30	Thr	Ile
Lys	Lys	Val 35	Ala	Gln	Val	Ala	Arg 40	Tyr	Gly	Ala	Lys	Ala 45	Leu	Leu	Thr
Thr	Lys 50	Glu	Glu	Val	Leu	Gln	Lys 55	Val	Asn	Ser	Ser 60	Cys	Glu	Trp	Val
Ala 65	Gln	Ala	Val	Ala	Ser 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Ser	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Leu	Ala 95	Ala	Glu
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala 110	Gly	Gln	Lys
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu 125	Arg	Ala	Asn	Ser
His 130	Leu	His	Gly	Ala	Ser 135	Gly	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro 155	His	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser 185	Tyr	Thr	Val	Asp	Phe 190	Asn	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu 205	Gly	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met 220	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn	Gly 255
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe 265	Ile	His	Gln	Cys	Lys 270	Pro	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln 280	Met	Leu	Glu	Leu 285	Leu	Ala	Gly	Ser
Ala 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His 300	Asp	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg 315	Cys	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ser	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn 345	Pro	Leu	Ile	Asp	Val 350	Ala	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn 360	Phe	Leu	Gly	Gln	Tyr 365	Ile	Gly	Thr	Ser

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470					475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Gly
545				550					555						560
Ser	Ile														

<210> 261

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 261

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgctgagc	ggtgaaccga	tttacggcgt	tacctcgggt		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatctggag	cgcgagcaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cgatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 262

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 262

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```


				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 263

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 263

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaggggctg accatcaaga aagtggtgca ggttgcgct 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgagga aaaccgccc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgagg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 264

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 264

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Gly Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 265

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 265

```
atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaat tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgagattc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 266

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 266

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 268
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 268
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Glu	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 269

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 269

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtggtta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgct 120
tatggtgcca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcggtggca tggcgcaagc gggttatcacc ccggacctgg cggcgagcgc gcagaataac 300
ctgatgcgtt atcacaaagc gggtgagcgc caaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```



```

ggtagcgagg ttgtagcgagg tattgtagcgagg aactgtagttt atgtagcgca gaacctgtagt 720
gtagctgagcc tgggtgtagca tgcgctggcg ctgtagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctgggagc tgctggcgagg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgc 1500
ctgagcccg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgcc 1560
agcgagagtc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgc 1620
ctgtagcgcg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgg 1680
agcatt 1686

```

<210> 270
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 270
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
           20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
           35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
           50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
           85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
           100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
           115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
           130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
           165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
           180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 271

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcggt 120
tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg cggatatcac cagcggtggc cgtattgttg aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 272

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 272

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325						330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485						490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Glu	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 273
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 273

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcg	ggttgcgcg	120
tatggtgcga	aggcgacgct	gaccaccaa	gaggaagtgc	tcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcggt		240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggacctgg	cggcgagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgcttcgtgcg		360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgctttg	cgaatttgg		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg		540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcgggc	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
ctgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgaccacag	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc		1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg		1560
agcgaggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	cgatatcac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 274
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 274

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Thr	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 275

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 275

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaa ttccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 276
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 276
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270

```


Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395				400			
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405				410						415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490							495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Ile	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 277

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 277

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgct 120
tatggtgcga aggcgtgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggtttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacatccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 278

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 278

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145	150								155				160				
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
				275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
His	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
				530					535					540			
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545					550					555							

<210> 279
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 279
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgatg 1680
agcatt 1686

<210> 280
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 280
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Met
545				550				555							560
Ser	Ile														

<210> 281

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 281

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcggcgta tcgaaacctt cctgaacgag ggctgacctg cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctga tcaccggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgag tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gctgtagcag tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accggttaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacag cggagcagtt taacaaaaac atcaacagcc agggtttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 282
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 282
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Arg Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagatccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 284

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 284

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Asp	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 285

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 285

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgct 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgta ca taccgggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggctc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 286

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 286

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135				140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185				190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345				350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg</

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 287
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 287
 atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
 tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
 ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtagacc cgacgcttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
 atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcgagcatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg cggatatcac cagcgtgggc cgtattgtta aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 288
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 288

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390							395				400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	His	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ile														

<210> 289

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 289

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaaagt gggtatcacc cgggacctgg cggcgagcgt gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtg 360
ggatatgctg tgcgtgcgaa cagccacctg tcgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt taacaaaaac atcaacagcc agggtttttg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 290

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 290

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu Ser Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```


290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Leu Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Ser Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Glu Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Ala				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 291

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 291

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga tacgccgctg accatcaaga aagtggcgca ggttgccgct 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 292

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 292

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Thr Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	545	550	555
Ser	Ile																	

<210> 293

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 293

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc ggttgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg tggggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 294

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 294

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

50		55		60											
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	Trp	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 296

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ser	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355						360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 297

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 297

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgctgagc	ggtgaaccga	tttacggcgt	tacctcgggt		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tggtcgtgctg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatctggag	cgcgagcagaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020


```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagtcg attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cgatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 298

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 298

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290				295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Ser	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 299

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 299

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagtggctg accatcaaga aagtggcgca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcggtaggca tggcgaaagt gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagctgct tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg ttagtaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 300

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 300

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Trp Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 301

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 301

```
atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcggtggca tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgacggg tattgaggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccc caccggggtc aaatctggag cgcgagcaga 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cgagcaggtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgacctgct gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaacg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cgacctgca actgtatctg gcgattaagg aagtgggttg taaaccgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg cggtatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 302

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 302

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 304
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 304
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Asp Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```


Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 305

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 305

```

atgatcattg cgagccagac ccaaaccttc accagcaa at ttccgcacac cgcgagcgac 60
agcgtggtta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggtgcgct 120
tatggtgcca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgcaagc gggtgagcgc ggtgaaccga tttacggcgt tacctcgggt 240
ttcggtggca tggcgaaagt gggtatcacc ccggacctgg cggcgagcgc gcagaataac 300
ctgatgcgtt atcacaagc gggtgagcgc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcgaa cagccacctg gggggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgacga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctgggagc tgctggcgggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 306

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 306

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu Gly Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 307

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcggtaggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttggg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 308

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 308

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100						105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Gly	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 309
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 309

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tcagcgtgt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcgggt		240
ttcggtaggca	tggcgaaagt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg		360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctgggttgg		540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
ctgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgaccacag	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc		1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg		1560
agcgaggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	cgatattcac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 310
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 310

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 311

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 311

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggc tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc gcgtgcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```



```

gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaa gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 312

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 312

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Arg Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520							525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530					535					540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ile																

<210> 313

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 313

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgct 120
tatggtgcga aggcgtgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaaagt gggtatcacc ccggacctgg cggcggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcgggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
gatgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 314

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 314

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145									150									155									160							
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly																			
																165									170									175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu																			
																180									185									190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu																			
																195									200									205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val																			
																210									215									220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu																			
																225									230									235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly																			
																245									250									255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro																			
																260									265									270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser																			
																275									280									285
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu																			
																290									295									300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr																			
																305									310									315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile																			
																325									330									335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn																			
																340									345									350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser																			
																355									360									365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp																			
																370									375									380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro																			
																385									390									395
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys																			
																405									410									415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr																			
																420									425									430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn																			
																435									440									445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg																			
																450									455									460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly																			
																465									470									475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp																			
																485									490									495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile																			
																500									505									510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Glu	Glu	Arg	Pro	Tyr	Ile	Trp																			
																515									520									525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala																			
																530									535									540
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val																			
																545																		

<210> 315
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 315
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgagc ggtgaaccga tttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggttatcacc cggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcaciaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgagc ggctgaccc cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcacgtgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 316
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 316
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Ser	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Thr	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 317

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 317

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aagtggcgca	ggttgcgcg	120
tatgggtgca	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagggtgt	taacagcagc	180
tgcgagtggg	tggcgcaagc	ggttgcgagc	ggtgaaccga	tttacggcgt	tacctcgggt	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctga	gcctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcaaa	cagccacctg	cacgggtgca	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttgg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgctggc	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcaaa	tgctgctggc	ctgcaggggc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaacgc	caccgggtgc	aaatctggag	cgcgagcaaa	840
atgctggagc	tgctggcggg	cagcgcgctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgcttgcg	gcagtatacc	960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttgc	ggtaacgcga	gctaccacgg	tggaacttc	1080
ctgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgctgctgct	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacag	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaac	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg	1440
gtgcaaacgc	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcgagggaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	cggatatcac	cagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 318
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 318
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcag gcaagtgggt 1680
agcatt 1686

```

<210> 320

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 320

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Arg	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 321

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 321

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaaga aagtggcgca gggttgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggttgcgagc ggtgaaccga ttacggcgt tacctcgggt 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacag cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgca gggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 322

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 322

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Lys Lys Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Ser Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100				105				110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
			275				280				285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Ser	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
			450				455				460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470				475				480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485				490				495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500				505								

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 323
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 323
 atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcgatg aggtggccca gggtgcgcgt 120
 tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgaacgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac gacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg cggatatcac cagcgtgggc cgtattgtta aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 324
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 324

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asp	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Asn	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555							560
Ser	Ile														

<210> 325

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 325

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgat aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgagt ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc cggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctggttgg 540
ctgaacgaca gttataaccg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```



```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtggttgg taaaccgccg 1560
agcgaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 326

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 326

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asp Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Val Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Pro Pro Ser Glu Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Ala				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 327

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 327

```

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgaacgc gggtgagagt ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgactg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg tgtgccgccg 1560
agcgaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcca gagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 328

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 328

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Asn Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245				250						255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Val	Pro	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530					535					540					
Asp	Ile	Gln	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 329

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 329

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaatg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccaataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcgaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgccactg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaagaac gtccgtatat ctggaacgac gacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcca gagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 330

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 330

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Leu	Ala	Ala 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Ala 285	Gly	Ser	
Ala 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ser	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu 335	Ile	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Val	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr 430	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala 445	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 332

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Asn	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 333

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 333

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggccca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tggtcgtgcg		360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctgggttgg		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 334

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 334

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 335

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 335

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgatg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgagt ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaat tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctgggag tgctggcggg cagcgactg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggtgg tgtgccgccg 1560
agcgaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcg cggatatcca gagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 336

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 336

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asp Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Val	Pro	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520						525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
						535					540				
Asp	Ile	Gln	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 337

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 337

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtggtta ttgtgggtga taagccgctg accatcaaga aggtggcca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgaacgc gggtgcgagt ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcactg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgagggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg cggtatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 338

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 338

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Asn	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340						345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 340
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 340
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Ala Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 341

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 341

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatggtgcca aggcgctgct gaccacaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgaggc gggtgagagt ggtgaaccga tttacggcgt taccactggc 240
ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcgagcgt gcagaataac 300
ctgatgcgtt atcacaagc gggtgaggc caaagctga gcctggcgga tgttcgtgctg 360
ggatgctgct tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccgggtg gctgggtggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgtagcgagg tattgaggcg aactgagttc atgtagcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaacgc caccggggtc aaatctggag cgcgcagcaa 840
atgctgggagc tgctggcgagg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcggtagc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 342
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 342
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 343

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcggt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatga tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaggaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 344

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 344

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 345
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 345

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaaga	aggtggccca	ggttgcgcg	ggttgcgcg	120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaagc	ggttgcgaaa	ggtgaaccga	tttacggcgt	taccactggt		240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgcttcgtgcg		360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttgg		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttgg		540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaca		840
atgctggagc	tgctggcggg	cagcgactcg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacgt	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggttaaca	gcacatgcgc	gctgctgacc	ttctacggca	acagcctgac	cgatcgcttc		1320
ccgacccacg	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt		1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg		1560
agcgaagaac	gtccgtatat	ctggaacgac	gacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	aggatatcca	gagcggtggc	cgtattgtta	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 346
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 346

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Lys	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Gln	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 347

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 347

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgatg aggtggccca ggttgcgctg 120
tatggtgcga aggcgtgctg gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaacgc ggttgcgagt ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccc caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcgga cagcgactg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaaccgccg 1560
agcgaagaac gtccgtatat ctggaacgac gacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 348

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 348

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asp Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Asn Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```



```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacgggtcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgcactg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaagaac gtccgtatat ctggaacgac gacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 350

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 350

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 351
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 351
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgagt ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgctg attcgtgac agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 352
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 352
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355						360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 353

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 353

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taaccgcgtg	accatcaagg	aggtggccca	ggttgcgcg	120
tatgggtgca	aggcgctgct	gaccaataaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgagagt	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctga	gcctggcgga	tgcttcgtgcg	360
ggtatgctgc	tgcgtgcaaa	cagccacctg	cacgggtgca	gcgggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacagcttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcgggc	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcaaa	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatctggag	cgcgagcaaa	840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgcttgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaat	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacgt	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaac	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgcttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcgaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 354
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 354
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Asn Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 356

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 356

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asp Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Ser Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 357

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 357

```
atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcgatg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcggg tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgac agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 358

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 358

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asp Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

100						105						110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
			275				280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 359
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 359
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca gggtgcgcgt 120
 tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgagt ggtgaaccga ttacggcgt taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagcgcactg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
 agcgaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
 ctgatcgcgg cggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 360
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 360

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Ser	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 361

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 361

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccaataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc cggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctggttgg 540
ctgaacgaca gttataaccg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcca gagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 362

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 362

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Val Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Glu Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Gln Ser Gly Gly Arg Ile Val Lys Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 363

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 363

```

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc cggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcga cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 364

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 364

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 365

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 365

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaacgc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccttg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcactg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcgaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 366

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 366

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Asn	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Leu	Ala	Ala 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg 125	Ala	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Ala 285	Gly	Ser	
Ala 290	Leu	Ile	Arg	Asp	Glu 295	Leu	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ser	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu 335	Ile	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Val	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr 430	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485					490					495					
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505					510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp				
			515				520						525						
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala				
			530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
						550				555					560				
545																			
Ser	Ile																		

<210> 367

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 367

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagcgcactg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 368

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 368

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355						360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 369

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 369

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggccca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccaataaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgagcgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg		360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagcgcactg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgtttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaagaac gtccgtatat ctggaacgac gacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 370

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 370

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290				295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Glu	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 371

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 371

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagcgactg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg cggatatcac cagcggtggc cgtattgtta aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 372

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 372

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Ala	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520						525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Ala
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Lys	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 373

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 373

```
atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca gggtgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcgaggct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaga 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatattac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 374

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 374

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 376
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 376
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 377

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 377

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca gggtgcgctg 120
tatggtagca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggc taacgcgagc 180
tgcgagtggg tggctcaggc gggtgcaag ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgctggc caaagctga gcctggcgga tgttcgtgcg 360
ggtagctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggtggc 540
ctgaacgaca gttataccgt tgattttaac ggagaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg ttgtagcgagg tattgtagcgagg aactgtagttc atgtagcgca gaacctgtagt 720
gtagctgagcc tgggtgtagca tgcgctggcg ctgtagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggcgagg cagccgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgcc 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgtagcgagg aggatatac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 378
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 378
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Thr Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 379

```
atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcggt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgctcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgcg cgtactgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 380

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 380

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Arg	Val	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 381
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 381

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggcca	ggttgcgct	120	
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180	
tgcgagtggg	tgaaccaggc	ggttgcggaag	ggtgaaccga	tttacggcgt	taccactggg	240	
ttcggatggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300	
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg	360	
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420	
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgcttg	cgaatttggt	480	
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggtggg	540	
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600	
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660	
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720	
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780	
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa	840	
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac	900	
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960	
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020	
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080	
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140	
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200	
gctagcctgg	tgggtaacgt	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260	
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320	
ccgaccacag	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380	
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440	
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500	
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560	
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620	
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680	
agcatt						1686	

<210> 382
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 382

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Asn	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 383

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 383

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggctcaggc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagctgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 384

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 384

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
		290				295					300					
Gln	Leu	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355				360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390						395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435				440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
		450			455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500				505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515				520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
		530				535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550						555					560	
Ser	Ile															

<210> 385

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 385

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatggtacga aggcgtgctg gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggctcaggc gggtgcgaag ggtgaaccga ttacggcgct taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagctgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 386

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 386

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Thr Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Gln	Leu	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550												

<210> 387
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 387
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 388
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 388
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr	
		35					40					45				
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340				345						350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355						360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 389

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 389

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggccca	ggttgcgctg	120
tatggtgcga	aggcgtgctg	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctga	gcctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagctgat	ccaagatcgt	tacagcctgc	gttgcttgcg	gcagtatacc	960
ggcccattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacgt	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 390
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 390
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Leu Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagctgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 392

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 392

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Thr Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Leu	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 393

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 393

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggctcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgtggg atcacaaagc gggtgcgggc caaaagctga gcctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgac agctggatgg tagccacgac 900
taccgtggcg aacagctgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgtgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 394

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 394

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Trp Tyr His Lys Ala Gly Ala Gly Gln Lys
```

100						105						110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Leu	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					46				

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 395
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 395
 atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca agttgcgcgt 120
 tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagggtgt taacagcagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt acgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacg 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcgtgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 396
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 396

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 397

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 397

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccga tgttgcgctg 120
tatgggtgcga aggcgctgct gaccaataaa gaggaagtgc tgcagggtgt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcgga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataaccg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc acgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacg 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac agccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 398

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 398

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Asp Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asn Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Val Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Thr Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Gln Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 399

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 399

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgaacgc gggtgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttc acgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 400

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 400

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555
Ser	Ile																	

<210> 401

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 401

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccga tgttgcgctg 120
tatggtgcga aggcgctgct gaccaataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg aaaaagctga gcctggcgga tgttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc acgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacct cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac agccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa tcaagtgggt 1680
agcatt
```

<210> 402

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 402

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Asp Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Leu	Ala	Ala 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Lys	Lys	
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala 285	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ser	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu 335	Ile	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu	Thr 390	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Val	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys	
Gly	Leu	Gln	Ile	Thr 420	Gly	Asn	Ser	Ile	Met 425	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro 440	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 404

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Asn	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355						360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370					375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505						510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 405

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 405

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggcca	agttgcgcgt		120
tatggtgcga	aggcgctgct	gaccaataaa	gaggaagtgc	tgcagggtgt	taacagcagc		180
tgcgagtggg	tggcgaacgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aaaaagctga	gcctggcgga	tgttcgtgcg		360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaacc	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	acgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatctggag	cgcgagcaa		840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacg 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac agccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa tcaagtgggt 1680
agcatt
1686

```

<210> 406

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 406

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asn Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Asn Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Gln	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 407

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 407

atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccga tgttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggca tggcgaaagt gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttc acgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa tcaagtgggt 1680
agcatt
1686

```

<210> 408

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 408

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Asp Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 409

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 409

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggcca agttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taaacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcga cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta taccgggtgc gctggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga taccgcgc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgcg aactgcgtt acgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcga tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgac agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaagg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgacctgc gtagcattga aatcttcag caatatatt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcaatgt 1500
ctgagcccg cgacctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 410

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 410

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgagg aggatatacac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 412
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 412
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Asp Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 413

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 413

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccga tgttgcgctg 120
tatgggtgca aggcgctgct gaccaataaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgaacgc gggtgcaag ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc aaaaagctga gcctggcgga tgttcgtgctg 360
ggatgctgct tgcgtgcaag cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccgggtg gctgggtggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg ttgtagcgagg tattgtagcgagg aactgtagggg acgatgtagca gaacctgtagg 720
gtagctgagcc tgggtgtagca tgcgctgtagg ctgtagggggc tgaacggtagc caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcgagg cagccgctg attcgtgagc agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctgtagc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgtagc gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgt 1500
ctgagcccg cgacctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgtagcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 414
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 414
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Asp Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 415

```
atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca agttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctga gcctggcgga tgcttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc acgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 416

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 416

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 417
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 417

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggccca	ggttgcgcg	ggt	120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcgagg	ggttgcggaag	ggtgaaccga	tttacggcgt	taccactggt		240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgcttcgtgcg		360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacacgtttg	cgaatttgg		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg		540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacct	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgacccacg	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt		1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg		1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	tgacgtgggt		1680
agcatt							1686

<210> 418
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 418

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Asp	Val	Val
545					550				555						560
Ser	Ile														

<210> 419

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 419

```

atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca agttgcgcgt 120
tatggtgcga aggcgtgct gaccaataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaacgc ggttgcgaa ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc acgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 420

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 420

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505					510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 421

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 421

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccga tgttgcgctg 120
tatggtgcga aggcgtgctg gaccaataaa gaggaagtgc tgcagggtgt taacagcagc 180
tgcgagtggg tggcgaacgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc aaaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgagc ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggtttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgagc tgatgaccgg tattgcggcg aactgcgttc acgatgcgca gaacctgctg 720
gctgtagacc tgggtgagca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacct cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatattcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 422

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 422

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Asp Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asn Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550												

<210> 423
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 423
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca agttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc acgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgctg attcgtgac agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac agccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatcac cagcggtggc cgtattgttc aggcgatcga ggacgtgggt 1680
agcatt 1686

<210> 424
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 424
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
	275						280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Gln	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Glu	Asp	Val	Val
545				550				555						560	
Ser	Ile														

<210> 425

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 425

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccga tgttgcgctg 120
tatgggtgca aggcgctgct gaccaataaa gaggaagtgc tgcagggtgt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcgga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgctg tgatgaccgg tattgcggcg aactgcgttt acgatgcgca gaacctgctg 720
gctgtagctg tgggtgcaac tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgctg aggatattac cagcggtggc cgtattgttc aggcgatcga gcaagtgggt 1680
agcatt

```

<210> 426
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 426
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Asp Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asn Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
ctgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggtttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaaacg 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcga ggacgtggtt 1680
agcatt 1686

```

<210> 428

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 428

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Asp Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Leu	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Glu	Asp	Val	Val	545	550	555	560
Ser	Ile																		

<210> 429

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 429

```
atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg accatcaagg aggtggccca agttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgcgtgacgg tattgcggcg aactgcgttt acgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgac agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatcac caagggtggc cgtattgttc aggcgatcaa tgacgtggtt 1680
agcatt 1686
```

<210> 430

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 430

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
```

			100					105				110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala	Ile Asn Asp Val Val			
545	550	555	560	
Ser Ile				

<210> 431
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 431

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggccca	agttgcgcgt		120
tatggtgcca	aggcgctgct	gaccactaaa	gaggaagtgc	tgacagaagg	taacagcagc		180
tgcgagtggg	tgccgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcgggtggca	tgccgaacgt	ggttatcacc	ccggacctgg	cgccggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg		360
ggtatgctgc	tgcggtgcga	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccc	ctggcggtaca	tcaccggtgc	gctgggttgg		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	acgatgcgca	gaacctgctg		720
gcgctgagcc	tggtgctgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatctggag	cgcgagcaa		840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc		1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tggtgaacgt	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac		1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgttttgg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt		1500
ctgagcccgg	cgaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg		1560
agcaaagaac	agccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 432
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 432

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Gln	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 433

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 433

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagggtgt taacagcagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc cgggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataaccg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt acgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa tcaagtgggt 1680
agcatt 1686

```

<210> 434

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 434

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Val Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 435

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 435

```

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcggtggca tggcgaacgt gggtatcacc cggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc tgggtcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcga cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg gctgcagatt 1260
tcgggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 436

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 436

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Ser	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 437

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 437

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gacctataa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagcgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaaac tgggtgcggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgata tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcgt cgtaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacct cgaccgtccg gttaacatgg gcctgaaggc gctgcagatt 1260
gcgggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 438

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 438

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```


	50					55					60				
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Leu	Ala	Ala 95	Glu
Leu	Gln	Asn	Asn	Leu 100	Met	Arg	Tyr	His 105	Lys	Thr	Gly	Ala	Gly	Gln	Lys
Leu	Ser	Leu	Ala	Asp 115	Val	Arg	Ala	Gly 120	Met	Leu	Leu	Arg	Ala	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu	Leu 140	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala	Leu 200	Lys	Leu	Leu	Gly	Leu 205	Glu	Pro	Leu
Glu	Leu 210	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn	Gly 255
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Ala	Gly	Ser
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp	Arg 310	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ser	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
Met	Asp 370	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly 405	Asn	Val	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys
Ala	Leu	Gln	Ile 420	Ala	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln	Asn 450	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 440

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Ala	Leu	Gln	Ile	Ser	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 441

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 441

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggccca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaaac	tgggtgcgggc	caaaagctga	gcctggcgga	tggtcgtgcg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtata	tcaccgggtg	gctgggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcgt cgtaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 442

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 442

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Thr Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 443

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 443

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgtggt atcacaaagc tgggtgcgggc caaaagctga gcctggcgga tgttcgtgctg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgata tcaccgggtg gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaat tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg gctgcagatt 1260
tcgggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcaggtt caaccaaacc atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 444

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 444

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Trp Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Ser	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 445

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 445

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggcca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taaacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctgtcgtata tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaagg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 446

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 446

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5				10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile	
			20					25					30			
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr	
		35					40					45				
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ser	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 448
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 448
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Trp Tyr His Lys Thr Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Ala	Leu	Gln	Ile	Ser	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 449

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 449

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggcca ggttgcgcgt 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgtggt atcacaaagc tgggtgcggc caaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtata tcaccgggtg gctgggtgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctgggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 450

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 450

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Trp Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 451

```
atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcggt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt ttatgaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 452

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 452

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```


Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Phe	Met	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 453
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 453

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggcca	ggttgcgcgt		120
tatggtgcga	aggcgtgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcggatggc	tggcgaacgt	ggttatcacc	ccggacctgg	cggcggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgcttcgtgcg		360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacacgtttg	cgaatttggg		480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaca	tcaccgggtgc	gctgggttgg		540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgaattg	cggacgggat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacgt	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgacccacg	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt		1500
ctgagcccgc	gtaccctgca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg		1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	aggatatcac	cagcgggtgg	cgtattgttc	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 454
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 454

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 455

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 455

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgctgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 456

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 456

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225         230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245         250         255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260         265         270

```

Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350
 Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser
 355 360 365
 Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp
 370 375 380
 Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro
 385 390 395 400
 Ala Ser Leu Val Gly Asn Val Asp Arg Pro Val Asn Met Gly Leu Lys
 405 410 415
 Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr
 420 425 430
 Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn
 435 440 445
 Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg
 450 455 460
 Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly
 465 470 475 480
 Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp
 485 490 495
 Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile
 500 505 510
 Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp
 515 520 525
 Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu
 530 535 540
 Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ile

<210> 457

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 457

atgatcattg cgagccagac ccaaaccttc accagcaaatt ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
 tatggtgcga aggcgtgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgca gcgggtatccg tctggagctg 420
attcagcgta tcgttacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggtttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 458

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 458

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 459
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 459
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgag tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag tattatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 460
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 460
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 461

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 461

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgttgt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gtagctgagc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattgttac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 462
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 462
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 464

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 464

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 465

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 465

```
atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
gttgagtggg tggcgagggc gggtgcaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcggg tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 466

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 466

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```


			100					105				110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530		535		540
Asp Ile Thr Ser Gly	Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val		
545	550	555	560	
Ser Ile				

<210> 467
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 467
 atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca gggtgcgcgt 120
 tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggca atcagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 468
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 468

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Asn
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 469

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 469

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgcttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataaccg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac ggaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 470

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 470

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Leu Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 471

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 471

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg aagccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 472

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 472

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Lys	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245					250						255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
		260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345						350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355						360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370				375						380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420					425						430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 473

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 473

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gacctataa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagcgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagtgcgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgagtgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 474

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 474

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

	50					55					60				
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Leu	Ala	Ala 95	Glu
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg 125	Ala	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	Ser 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser 185	Tyr	Thr	Val	Asp	Phe 190	Asn	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met 220	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His 235	Asp	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln 280	Met	Leu	Glu	Leu	Leu 285	Ala	Gly	Ser
Arg 290	Leu	Ile	Arg	Asp	Glu 295	Leu	Asp	Gly	Ser	His 300	Asp	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg 315	Cys	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ser	Glu	Ile 330	Ala	Lys	Gln	Ile 335	Glu	Ile
Glu	Ile	Asn 340	Ser	Val	Thr	Asp	Asn 345	Pro	Leu	Ile	Asp	Val 350	Ala	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn 360	Phe	Met	Gly	Gln	Tyr 365	Ile	Gly	Thr	Ser
Met	Asp	Arg 370	Leu	Arg	Tyr 375	Tyr	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu 390	Leu	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val 405	Gly	Asn	Val	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu 430	Thr	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg 440	Phe	Pro	Thr	His 445	Ala	Glu	Gln	Phe	Asn
Gln	Asn 450	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala 460	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe 470	Gln	Gln	Tyr	Ile	Ala 475	Ile	Ala	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 476

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Lys	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 477

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 477

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggccca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggacctgg	cgaaggagct	gcagaataac		300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tggtcgtgctg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatctggag	cgcgagcaaa		840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 478

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 478

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490						495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530			535						540							
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 479

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 479

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tgatgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 480

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 480

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Met Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```


His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 481

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 481

```
atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca gggtgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggc taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cgagcaggtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgag taccagaaga attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 482

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 482

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgagg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 484
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 484
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Val Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455				460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535				540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ile														

<210> 485

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 485

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg agtatcaagg aggtggcca ggttgcgcgt 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcgagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg ttgtagcgagg tattgtagcgagg aactgtagttc atgtagcgca gaacctgtagt 720
gtagctgagcc tgggtgtagca tgcgctggcg ctgtagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcgagg cagccgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgt 1500
ctgagcccg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgtagcgagg aggatatac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 486

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 486

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Ser Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 487

```
atgatcattg cgagccagac ccaaaccttc accagcaaatt tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggcca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtagga tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgac tgaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 488

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 488

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Thr	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 489

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 489

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcggt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagcgc gggtgcgaag ggtgaaccga ttacggcggt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacaa ggaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 490

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 490

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Lys	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 491

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 491

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcttggttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 492

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 492

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro Leu Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395					400			
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405				410						415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490							495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515				520							525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 493

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 493

```

atgatcattg cgagccagac ccaaaccttc accagcaaatt tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggcca ggttgcgct 120
tatggtgcga aggcgtgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggacctgg cggcggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctgcgtgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 494

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 494

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Leu Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```


145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Arg	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Leu	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550												

<210> 495
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 495
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggacctgg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgag tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatctggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccgttca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 496
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 496
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Leu	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355						360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Val	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 497

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 497

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggccca	ggttgcgctg	120
tatggtgcca	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgaatgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cggcggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	cagaagctga	gcctggcgga	tgcttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgtaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgctaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacgggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacgt	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
agtggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	cgaccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 498
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 498
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
actggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac aacgagcagg cgctggatga acacattgag 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 500

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 500

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 501

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 501

```
atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcga aggcgctgct gaccaataaaa gaggaagtgc tgcagaaggt taacgcgagc 180
tgcgagtggg tggcgaatgc ggttgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggca tggcgaacgt ggttatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgcgct atcacaaagc ggggtgcgggc aagaagctga gcctggcggga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
actggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 502

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 502

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
```

100						105						110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135					140				
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
			275				280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 503
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 503
 atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca gggtgcgcgt 120
 tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc aagaagctga gcctggcggg tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgtaacctt cctgaacgcg ggcgtagacc cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 actggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatcac cagcgtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 504
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 504

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555							560
Ser	Ile														

<210> 505

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 505

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagggtgt taactcgagc 180
tgcgagtggg tggcgaatgc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctga gcctggcgga tgcttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataaccg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
actggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacc 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 506

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 506

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Val Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Thr Leu Ser Pro Ala Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 507

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 507

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgaatgc gggtgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc cagaagctga gcctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
actggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 508

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 508

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```


Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 509

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 509

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taactcgagc 180
tgcgagtggg tggcgcaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgctgt atcacaaagc ggggtgcggg aagaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacct cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
agtggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 510

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 510

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Ala 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Leu	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Lys	Lys	
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu	Leu 140	Ile	Gln	Arg	Ile	
Val 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly	Leu 205	Glu	Pro	Leu	
Glu	Leu 210	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ser	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu	Thr 390	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Val	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys	
Gly	Leu	Gln	Ile	Ser	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro 440	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 512

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 513

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 513

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggccca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagggtgt	taacgcgagc		180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt		240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cggcggagct	gcagaataac		300
ctgatgcgct	atcacaaagc	gggtgcgggc	aagaagctga	gcctggcgga	tggtcgtgcg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgtaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa		840
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
agtggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 514

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 514

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Ser	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 515

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 515

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120


```

tatggtgcga aggcgctgct gaccaataaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcgagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc cagaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
actgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacc 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 516

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 516

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asn Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
					295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
					535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 517

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 517

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggcca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taaacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc cagaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta taccgggtgc gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggc tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaagg tctgcagatt 1260
actgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cgaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 518

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 518

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5				10					15				
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gcccgatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgagg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 520
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 520
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 521

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 521

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtggtta ttgtgggtga taagccgctg accatcaagg aggtggcca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagggtgt taactcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc aagaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
actggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacc 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 522

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 522

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 523

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccga cgttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc aagaagctga gcctggcgga tgttcgtgcg 360
ggtagctgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
agtggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacc 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac aaccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 524

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 524

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Asp Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Ala	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Ser	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Thr	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Gln	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 525
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 525

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	accatcaagg	aggtggccca	ggttgcgctg	120	
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tcgagggtgt	taacgcgagc	180	
tgcgagtggg	tggcgagcgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240	
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cggcggagct	gcagaataac	300	
ctgatgctgc	atcacaaagc	gggtgcgggc	aagaagctga	gcctggcgga	tgcttcgtgcg	360	
ggtatgctgc	tgctgagcaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420	
attcagcgta	tcgtaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggg	480	
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttgg	540	
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600	
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660	
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720	
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780	
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840	
atgctggagc	tgctggcggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac	900	
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960	
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020	
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080	
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140	
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200	
gctagcctgg	tgggtaacct	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260	
actggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320	
ccgacccacg	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380	
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440	
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500	
ctgagcccgg	cgacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg	1560	
agcaaagaac	gcccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620	
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680	
agcatt						1686	

<210> 526
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 526

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 527

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 527

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc cagaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
agtggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaaacc 1500
ctgagcccgg cgaccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 528

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 528

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350
 Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser
 355 360 365
 Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp
 370 375 380
 Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro
 385 390 395 400
 Ala Ser Leu Val Gly Asn Val Asp Arg Pro Val Asn Met Gly Leu Lys
 405 410 415
 Gly Leu Gln Ile Ser Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr
 420 425 430
 Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn
 435 440 445
 Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg
 450 455 460
 Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly
 465 470 475 480
 Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp
 485 490 495
 Ala Ser Gln Thr Leu Ser Pro Ala Thr Arg Gln Leu Tyr Leu Ala Ile
 500 505 510
 Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp
 515 520 525
 Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu
 530 535 540
 Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ile

<210> 529

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 529

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
 tatggtgcga aggcgtgct gaccaataaa gaggaagtgc tgcagaaggt taacgcgagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300


```

ctgatgcgct atcacaaagc ggggtgcgggc cagaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
agtggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 530

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 530

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asn Lys Glu Glu Val Leu Gln Lys Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Ser	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550												

<210> 531
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 531
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccga cgttgcgctg 120
tatgggtgca aggcgctgct gaccaataaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgctgc atcacaagc gggtgcgggc cagaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgag ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgctg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
actggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 532
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 532
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Asp	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Asn	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Ala	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355						360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 533

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 533

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc cagaagctga gcctggcgga tgctctgctg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcgga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gctgtagcgc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggcggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
agtggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacag cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatattac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 534
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 534
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat ttcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgag 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 536

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 536

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```


Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 537

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 537

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc ggttgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt ggttatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcggg tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 538

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 538

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100				105				110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
			450				455				460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470				475				480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485				490				495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500				505								

530	535	540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val	
545	550	555
Ser Ile		

<210> 539
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 539
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
 tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
 gtcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
 ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgcattgttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 540
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 540

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Val	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ile														

<210> 541

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 541

```

atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgctcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcatgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 542

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 542

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 543

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 543

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg tcgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcattgttg cgaatttggt 480

```



```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat ttcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgacccgtc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccagggtggtt 1680
agcatt 1686

```

<210> 544

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 544

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Ser Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

$\langle 210 \rangle$	545
$\langle 211 \rangle$	1686

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 545

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gacctataa gaggaagtgc tgcagaaggt taacagcagc 180
gtcagagtggg tggcgagcgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg ttagtaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttgtag cgcgagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgcgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 546

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 546

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
```

	50					55					60				
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala	Gly 120	Met	Leu	Leu	Arg	Ala 125	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala	Leu 200	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Ala	Gly	Ser
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp	Arg 310	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro 440	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 548

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Ser	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 549

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 549

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
gtcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg		360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcattgttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctgggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa		840
atgctggagc	tgctggccgg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaggtgggt 1680
agcatt
1686

```

<210> 550

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 550

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```


				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 551

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 551

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcgagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgcagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat ttcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 552

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 552

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 553

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 553

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgta ca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggc tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaagg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg ccacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccagggtggt 1680
agcatt 1686
```

<210> 554

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 554

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 556
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 556
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 557

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 557

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca ggttgcgcgt 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcattgttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```



```

ggtagcgagg tgatgacggg tattgaggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaa 1380
ctgacccgct gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccagggtggt 1680
agcatt

```

<210> 558

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 558

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 559

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgagtgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccaccctca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 560

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 560

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	Ser	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485						490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 561
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 561

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	tcgatcaagg	aggtggcca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgagcgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcggatggc	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgcttcgtgcg		360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgagtgtttg	cgaatttggg		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttgg		540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa		840
atgctggagc	tgctgcaggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgattg	cggacgggat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacct	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgacccacg	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt		1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg		1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	aggatatcac	cagcgacggc	cgtattgttc	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 562
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 562

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Ser	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	Ser	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 563

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 563

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg tcgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat ttcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 564

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 564

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Ser Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225         230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245         250         255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260         265         270

```


Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350
 Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser
 355 360 365
 Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp
 370 375 380
 Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro
 385 390 395 400
 Ala Ser Leu Val Gly Asn Val Asp Arg Pro Val Asn Met Gly Leu Lys
 405 410 415
 Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr
 420 425 430
 Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn
 435 440 445
 Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg
 450 455 460
 Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly
 465 470 475 480
 Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp
 485 490 495
 Ala Ser Gln Cys Leu Ser Pro Ala Thr Arg Gln Leu Tyr Leu Ala Ile
 500 505 510
 Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp
 515 520 525
 Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu
 530 535 540
 Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ile

<210> 565

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 565

atgatcattg cgagccagac ccaaaccttc accagcaaatt ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca ggttgcgctg 120
 tatggtgcga aggcgtgctg gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
 gtcgagtggg tggcgagcgc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat ttcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcca aagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 566

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 566

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Gln	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 567
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 567
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgagtgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatcac cagcgggtggc cgtattgttc aggcgatcaa ccaggtgggt 1680
agcatt 1686

<210> 568
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 568
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr	
		35					40					45				
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	Ser	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355						360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 569

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 569

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	tcgatcaagg	aggtggccca	ggttgcgctg	120
tatgggtgca	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcatgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctggccgg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacgggat	ttcggaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaat	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacgt	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	cagtatatatt	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcg	aggatatcac	cagcggcggc	cgtattgttc	aggcgatcaa	ccaggtggtt	1680
agcatt						1686

<210> 570
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 570
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Ser Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgag 1620
ctgatcgagg aggatatcca aagcggcggc cgtattgttc aggcgatcaa ccaggtggtt 1680
agcatt 1686

```

<210> 572

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 572

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Gln	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 573

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 573

```
atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgct 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
gtcgagtggg tggcgaggc ggttgcaag ggtgaaccga ttacggcgt taccactggc 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc ccatgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgact gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ttgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaggtggtt 1680
agcatt 1686
```

<210> 574

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 574

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

		100				105				110						
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
		130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145							150					155				
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
						165					170					
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
						180					185					
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
						195					200					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
						210					215					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225							230					235				
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
						245					250					
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
						260					265					
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
						275					280					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
						290					295					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305							310					315				
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
						325					330					
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
						340					345					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
						355					360					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
						370					375					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385							390					395				
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
						405					410					
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
						420					425					
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
						435					440					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
						450					455					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465							470					475				
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
						485					490					
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
						500					505					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
						515					520					
Asn																

530	535	540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val	
545	550	555
Ser Ile		560

<210> 575
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 575
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg tcgatcaagg aggtggccca gggtgcgcgt 120
 tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
 gtcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcggg tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgcattgttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcggcggc cgtattgttc aggcgatcaa ccagggtggtt 1680
 agcatt 1686

<210> 576
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 576

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Ser	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Val	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 577

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 577

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg accatcaagg aggtggccca gggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
gtcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 578

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 578

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```


290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 579

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 579

```

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcattgttg cgaatttgg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 580

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 580

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 581

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 581

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcattgttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg ttagtaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgcgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 582

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 582

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Ala 285	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ser	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu 335	Ile	
Glu	Ile	Asn 340	Ser	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr 430	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala 445	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 584

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Ser	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Val	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Ala	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370					375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 585

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 585

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg		360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa		840
atgctggagc	tgctggccgg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020


```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgct 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 586

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 586

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 587

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 587

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg tcgatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 588

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 588

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Ser Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
					295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 589

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 589

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtggtta ttgtgggtga taagccgctg tcgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcga cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacgtt cctgaacgcg ggcgtgacct cgcattgttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcccgc aactgcgttc atgatgcgaa gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag cagtattatg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcca aagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 590

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 590

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Ser	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Lys	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 592
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 592
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```


Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 593

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 593

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca ggttgcgcgt 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taacagcagc 180
gtcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcattgttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg ttgtagcgagg tattgtagcgagg aactgtagttc atgtagcgca gaacctgtagt 720
gtagctgagcc tgggtgtagca tgcgctggcg ctgtagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgt 1500
ctgagcccg ccacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgcc 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgtagcgagg aggatatac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 594

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 594

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 595

```
atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
gtcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgctcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcattgttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat ttcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg cgaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 596

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 596

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485						490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 597

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 597

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
gtcagtgagg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgctcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcattgttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacct cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatac cagcgcgggc cgtattgttc aggcgatcaa ccagggtggg 1680
agcatt

```

<210> 598

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 598

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Val	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 599

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 599

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gacctataaa gaggaagtgc tgcagaaggt taacagcagc 180
gtcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacgtt cctgaacgcg ggcgtgaccc cgagtgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```



```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag tactatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 600

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 600

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro Ser Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225         230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245         250         255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260         265         270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505					510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ile																

<210> 601

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 601

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg tcgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
gtcgagtggg tggcgaggc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcattgttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 602

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 602

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Ser Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 603
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 603
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgacccc cgcacgtttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgctaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 604
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 604
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355						360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 605

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 605

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtggtta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctga	gcctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcatgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctggccag	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tagcgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacgt	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	taaccaaaaac	atcaacagcc	agggttttgg	cagcgcgaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcaccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcgacggc	cgtattgttc	aggcgatcaa	ccaggtgggt	1680
agcatt						1686

<210> 606
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 606
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Ser Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccagtggtt 1680
agcatt 1686

```

<210> 608

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 608

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Ser Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 609

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 609

```
atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
gtcgagtggg tggcgagggc gggtgcaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cggcggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcggg tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacgtt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgacccc ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgac agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 610

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 610

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Ala Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 611
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 611
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
 tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
 ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacgtt cctgaacgcg ggctgacctc cgcattgttg cgaatttgg 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tagcgaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacgt cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatatcca aagcggcggc cgtattgttc aggcgatcaa ccagggtggt 1680
 agcatt 1686

<210> 612
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 612

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Ala	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Val	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Gln	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 613

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 613

```

atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
gtcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggatggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggatgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgagtgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataaccg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctggccgg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tagcgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```



```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ccaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 614

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 614

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Val Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro Ser Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Ala Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290						295						300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340				345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405				410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485				490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
		515				520							525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ile																

<210> 615

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 615

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac gatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgagg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 616

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 616

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 617

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 617

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagggcgt taacgcgagc 180
tgcgagtggg tggcgcgaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 618

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 618

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu	Thr 390	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr 430	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro 440	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln 470	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535						540							
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545					550					555					560				
Ser	Ile																		

<210> 619

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 619

```

atgatcattg cgagccagac ccaaaccttc accagcaaata tcccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtgggtcca agttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg atgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattgggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcggttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 620

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 620

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Val	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	Met	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 621

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 621

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagggcgt	taacgcgagc		180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt		240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac		300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tggtcgtgctg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	catggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgtaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttggt		540
ctgaacgaca	gttataacctg	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa		840
atgctggagc	tgctgcaggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgattg	cggacggtat	tcaagaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag tattatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 622

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 622

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Gln	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 623

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 623

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggtcgc ggttgccgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg atgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat ttcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 624

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 624

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Val Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	Met	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile			
	130					135					140							
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly			
145					150					155					160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly			
				165					170						175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu			
			180					185						190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu			
		195					200					205						
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210					215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu			
225					230					235					240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly			
				245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro			
			260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser			
		275					280						285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu			
	290					295					300							
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr			
305					310					315					320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile			
				325				330						335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn			
			340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser			
		355					360					365						
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp			
	370					375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro			
385					390					395					400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys			
				405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr			
			420					425					430					
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn			
		435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg			
	450					455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly			
465					470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp			
				485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile			
			500					505					510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp			
		515					520					525						
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu			
	530					535					540							
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val			
545					550					555					560			

Ser Ile

<210> 625

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 625

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggtcgc gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taaacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 626

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 626

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Val	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gcccgatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgagg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 628
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 628
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 629

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 629

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggtcca agttgcgcgt 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagaaagt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgacga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat ttcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 630

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 630

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Val Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 631

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc ggttgcgcggt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagatt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag tattatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 632

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 632

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485						490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 633
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 633

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtgggtcca	agttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tcagggcgct	taactcgagc		180
tgcgagtggg	tggcgagcgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac		300
ctgatgcgct	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg		360
ggtatgctgc	tgcgtgcgaa	cagccacctg	catggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgtaacctt	cctgaacgcg	ggcgtgaccc	cgacgctttg	cgaatttggg		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttgg		540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttggag	cgcgagcaaa		840
atgctggagc	tgctgcaggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgaattg	cggacgggat	ttcggaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc		1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgaccacag	cggagcagtt	taacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa		1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt		1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg		1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg		1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 634
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 634

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Val	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 635

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 635

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 636

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 636

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350
 Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser
 355 360 365
 Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp
 370 375 380
 Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro
 385 390 395 400
 Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys
 405 410 415
 Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr
 420 425 430
 Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn
 435 440 445
 Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg
 450 455 460
 Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly
 465 470 475 480
 Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp
 485 490 495
 Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile
 500 505 510
 Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp
 515 520 525
 Asn Asp Asp Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu
 530 535 540
 Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ile

<210> 637

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 637

atgatcattg cgagccagac ccaaaccttc accagcaaatt ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggtcgc ggttgccgct 120
 tatggtgcga aggcgtgct gaccactaaa gaggaagtgc tgcagaaagt taactcgagc 180
 tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggc 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300

```

ctgatgctgt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg catgggtcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 638

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 638

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Val Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145	150								155				160				
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555							

<210> 639
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 639
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tcaagaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 640
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 640
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
	275					280						285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Gln	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420				425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 641

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 641

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg catgggtgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca ca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat ttcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag tattatatcg gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgtgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```


<210> 642
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 642
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ser Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 644

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 644

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 645

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 645

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtgggtcca agttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctga gcctggcggg tggtcgtgcg 360
ggatatgctg tcggtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat ttcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 646

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 646

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Val Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100				105				110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450														

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 647
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 647
 atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggtcgc gggttgcgcgt 120
 tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaaagt taacgcgagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcggg tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg atgggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
 agcaaagaac gcccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 648
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 648

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Val	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	Met	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 649

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 649

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtgggtcca agttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaagt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacct cgcacgtttg cgaatttgg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 650

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 650

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Val Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asp Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 651

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 651

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagggcgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag tattatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 652

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 652

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 653

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 653

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc gggttgcgct 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagggcgt taacgcgagc 180
tgcgagtggg tggcgcgaggc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat ttcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac tgccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 654

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 654

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln 285	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ser	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu	Thr 390	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met 425	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 656

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 657

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 657

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	agttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaaagt	taacgcgagc		180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tggtcgtgcg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	catggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa		840
atgctggagc	tgctgcaggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tcaagaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac tgccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 658

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 658

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225         230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Gln	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Leu	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 659

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 659

atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg acgatcaagg aggtggtcca agttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 660

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 660

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Val Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
					295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
					535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 661

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 661

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggtcgc gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagggcgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgta ca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat ttcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 662

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 662

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Val	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 664
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 664
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535				540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 665

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 665

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggtcgc ggttgcgct 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactgg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tcaagaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 666

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 666

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Val Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 667

```
atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg atgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tcaagaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 668

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 668

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	Met	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Gln	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485						490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 669

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 669

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggctgc ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagcgc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg catggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtaacctt cctgaacgcg ggctgacccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat ttcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accggttaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagatt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag tattatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gcccgatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 670

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 670

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Val	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ser	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 671

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 671

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg tgttgaaccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgct 1620
ctgatcgcgg aggatatcac caaggatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 672

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 672

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325					330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470					475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Val	Glu	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 673

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 673

```

atgatcattg cgagccagac ccaaaccttc accagcaaatt ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaagg aggtggccca ggttgcgct 120
tatggtgcga aggcgacgct gaccgataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc ggttgcggaag ggtgaaccga ttacggcgt taccactggt 240
ttcgggtggca tggcgaaact ggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgca gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgagc ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggtttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgagc tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gctgtagacc tgggtgagca tgcgctggcg ctgcaggggc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagaaccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatattac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 674

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 674

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Thr Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Glu	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550												

<210> 675
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 675
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcga aggcgcgcct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggcgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacccc cgctggtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 676
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 676
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr	
		35					40					45				
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	Leu	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340				345						350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355						360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 677

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 677

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taaaccgctg	acgatcaatg	aggtggccca	ggttgcgcgt		120
tatgggtgcga	aggcgacgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctga	gcctggcgga	cgttcgtgcg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacgggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctggttggg		540
ctgaacgaca	gttataaccgt	tgatttttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa		840
atgctggagc	tgctgcaggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc		960
ggcccgaattg	cggacgggtat	tgcggaaatc	gcgaagcaaa	tcgagatcga	aatcaacagc		1020
gtgaccgaca	acccgctgat	cgatgtttgcg	ggtaacgcga	gctaccacgg	tggaacttc		1080
atgggccaagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg		1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg		1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt		1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc		1320
ccgaccacg	cggagcagtt	taaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac		1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg		1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt		1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggtgg	tggtgcaccg		1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagt	cgctggatga	acacattgcg		1620
ctgatcgcg	aggatatcac	caaggatggc	cgtattgttc	aggcgatcaa	ccaagtgggt		1680
agcatt							1686

<210> 678
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 678
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Thr Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaacctccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgag 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 680

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 680

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 681

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 681

```
atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcga aggcgctgct gaccgataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcggg tggtcgtgcg 360
ggatatgctg tcggtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgac agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaacctccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 682

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 682

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185				190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 683
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 683
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taaaccgctg acgatcaatg aggtggccca gggtgcgcgt 120
 tatgggtgca aggcgacgct gaccgataaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggg 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcaccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatcac cagtgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 684
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 684

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Thr	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 685

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 685

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgctcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttgg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttgg 540
ctgaacgaca gttataaccg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaggatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 686

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 686

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 687

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 687

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgacgct gaccactaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtggttgg taaagcaccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 688

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 688

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Thr Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 689

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 689

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagcgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtagtgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta taccgggtgc gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg ttagtaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgcgcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcaccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagtgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 690

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 690

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg 125	Ala	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu	Leu 210	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn 350	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile	Met 425	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro 440	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln 470	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 692

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355						360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 693

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 693

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taaaccgctg	acgatcaatg	aggtggccca	ggttgcgcgt		120
tatggtgcga	aggcgacgct	gaccgataaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctga	gcctggcgga	tgttcgtgcg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa		840
atgctggagc	tgctgcaggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtgggttg taaagaaccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaggatggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 694

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 694

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Thr Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360					365						
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375				380								
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455				460								
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490						495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Glu	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530			535					540								
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 695

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 695

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaatg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgacgct gaccgataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcaccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 696

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 696

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Thr Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 697

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 697

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaagg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaacctccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatcac cagtgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 698

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 698

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagtgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 700
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 700
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 701

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 701

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgtg acgatcaatg aggtggcca ggttgcgcgt 120
tatggtgcga aggcgcgcct gaccgataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg ttgtagcgagg tattgtagcgagg aactgtagttc atgtagcgca gaacctgtagt 720
gtagctgagcc tgggtgtagca tgcgctggcg ctgtagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgtaggg cagccgctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgcc 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgtagcgagg aggatatcac cagttagtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 702

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 702

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 703

```
atgatcattg cgagccagac ccaaacccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaatg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaacctccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 704

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 704

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 705

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 705

```

atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgcgcct gaccgataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgctcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg tggtgaaccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatcac caaggatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 706

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 706

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Val	Glu	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 707

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 707

```

atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgcgcct gaccgataaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcaccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgct 1620
ctgatcgagg aggatatcac cagtgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 708

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 708

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225         230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245         250         255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260         265         270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
	275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405				410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 709

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 709

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaaccgctg acgatcaatg aggtggccca ggttgcgct 120
tatggtgcga aggcgacgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga ttacggcgt taccactggt 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagaaccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 710

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 710

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Thr Leu Thr
35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Glu	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 711
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 711
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccactg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctga gcctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgcacgtttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
gcaatcgcgg aggatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 712
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 712
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
	275						280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355						360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 713

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 713

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctga gcctggcgga tgctctgctg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgacccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgag tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gctgtagcag tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgaatt cgagcggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgtgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 714
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 714
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 716

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 716

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Arg Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 717

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 717

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccactg acgatcaagg aggtggccca ggttgcgcg 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctga gcctggcggg tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagacc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 718

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 718

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

100						105						110			
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 719
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 719
 atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taaggagctg acgatcaagg aggtggccca gggtgcgcgt 120
 tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
 tgcgagtggg tggcgaacgc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc aagaagctga gcctggcggg tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
 taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620
 ctgatcgcgg aggatattac cagcgggtggc cgtattgttc aggcgatcaa tcaagtgggt 1680
 agcatt 1686

<210> 720
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 720

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Glu	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Asn	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 721

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 721

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctga gcctggcgga tgcttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa tcaagtgggtg 1680
agcatt 1686

```

<210> 722

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 722

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 723

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 723

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctga gcctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagccc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcga acaagtgggtg 1680
agcatt 1686

```

<210> 724

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 724

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Ala	Arg	Pro	Tyr	Ile	Trp	515	520	525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Glu	Gln	Val	Val	545	550	555
Ser	Ile																	

<210> 725

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 725

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tcccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taaggagctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc aagaagctga gcctggcgga tgttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taaccaaacc atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 726

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 726

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Glu Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```


	50					55					60				
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Lys	Lys
Leu	Ser	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Gln 285	Gly	Ser
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu 335	Ile
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu	Thr 390	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr 430	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro 440	Thr	His	Ala	Glu	Gln 445	Phe	Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln 470	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 728

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Gly	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Asn	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 729

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 729

atgatcattg	cgagccagac	ccaaaccttc	accagcaa	at	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taaggagctg	acgatcaagg	aggtggcca	ggttgcgcgt		120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaggt	taacagcagc		180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg		240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac		300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aagaagctga	gcctggcgga	tggtcgtgcg		360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg		420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt		480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccgggtg	gctgggttggt		540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg		600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac		660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg		720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc		780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa		840
atgctggagc	tgctgcaggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac		900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc		960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc		1020

```

gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagacc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 730

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 730

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Glu Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 731

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 731

atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggtta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctga gcctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtataag gcgattaagg aagtgggttg taaagcgccg 1560
gataaagcac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
gcaatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa tgacgtggtg 1680
agcatt
1686

```

<210> 732

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 732

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Lys	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Ala	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Asp	Val	Val
545					550					555					560

Ser Ile

<210> 733

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 733

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaagt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgagcaa 840
atgctggatc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 734

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 734

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Asp	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 736
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 736
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 737

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 737

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgct 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg ttgtagcgagg tattgtagcgagg aactgtagttc atgtagcgca gaacctgtagt 720
gtagctgagcc tgggtgtagca tgcgctggcg ctgtagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggaac tgctgtaggg cagccgctg gttcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgcc 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgtagcgagg aggatatac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 738

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 738

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 739

```
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaagt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactgg 240
ttcggtagga tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttgg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgaatt cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg tcaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 740

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 740

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```


Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 741

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 741

```

atgatcattg cgagccagac ccaaaccttc accagcaaata ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcggt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcggt taacagcagc 180
tgcgagtggg tggcgagcgc gggtgcgaag ggtgaaccga ttacggcggt taccactgggt 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttgggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtgggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctgcctcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggatc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 742

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 742

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Asp	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 743

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 743

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaagt taacagcagc 180
tgcgagtggg tggcgcaggc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgt cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggatc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgct 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 744

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 744

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```



```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacagtgtt cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggatc tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 746

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 746

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Asp	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 747
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 747
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggaac tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg tcaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 748
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 748
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 749

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 749

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatgggtgca	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaagt	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	attcgtgacg	agctggatgg	tagccacgac	900
taccgtggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacgggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 750
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 750
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg tcaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 752

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 752

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 753

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 753

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaaagt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctgtcgc tgctgcaggg cagccaactg atccgtgac agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgtgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 754

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 754

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```


100						105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Ser	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ser				

<210> 755
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 755
 atgatcattg cgagccagac ccaaacccttc accagcaaatttccgcacac cgcgagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
 tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaagt taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctcgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
 atgctggatc tgctgcaggc cagccaactg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg tcaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 756
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 756

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Asp	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 757

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 757

```

atgatcattg cgagccagac ccaaaccctt accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaagt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggaac tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 758

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 758

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		560
Ser Ser				

<210> 759

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 759

```

atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagaaaagt taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggaac tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg tcaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 760

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 760

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ser															

<210> 761

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 761

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gacctataa gaggaagtgc tgcagaaagt taacagcagc 180
tgcgagtggg tggcgcgagg gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg ttagtaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggatc tgctgcaggg cagccaactg gtccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 762

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 762

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg 125	Ala	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser 185	Tyr	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln 280	Met	Leu	Asp	Leu	Leu 285	Gln	Gly	Ser	
Gln 290	Leu	Val	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu 335	Ile	
Glu	Ile	Asn 340	Ser	Val	Thr	Asp	Asn 345	Pro	Leu	Ile	Asp	Val 350	Ala	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile 365	Gly	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu 430	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala 445	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545				550					555					560					
Ser	Ile																		

<210> 763

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 763

```

atgatcattg cgagccagac ccaaaccctt accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaaagt taacagcagc 180
tgcgagtggg tggcgcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg tcaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 764

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 764

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Phe	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 765

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 765

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggcca	ggttgcgcgt	120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaaagt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgt	cgctggcgga	tggtcgtgcg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctggttggg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	ttgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggatc	tgctgcaggg	cagccgcctg	gtccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 766

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 766

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Leu Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Asp	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535					540							
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 767

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 767

atgatcattg cgagccagac ccaaaccttc accagcaaatttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgt cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg tcaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 768

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 768

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```


His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 769

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 769

```
atgatcattg cgagccagac ccaaaccttc accagcaa at tccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaagt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgta ca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggatc tgctgcaggg cagccaactg gtccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 770

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 770

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Asp	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 772
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 772
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Val Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 773

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 773

```

atgatcattg cgagccagac ccaaaccttc accagcaa at ttccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgct 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagaaagt taacagcagc 180
tgcgagtggg tggcgaggc gggtgccaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgacga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 774

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 774

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 775

```
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaggt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgcttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 776

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 776

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 777

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 777

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagaaagt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgctcgctgc 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggaac tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgaatt cgagcggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cgagcagatt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg tcaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 778

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 778

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Lys	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 779

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 779

```

atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gacctataa gaggaagtgc tgcagaaagt taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgt cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgaggcg aagaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt taacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgct 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 780

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 780

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390						395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550					555						560	
Ser	Ile															

<210> 781

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 781

```

atgatcattg cgagccagac ccaaaccttc accagcaaatt ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgtgctg gaccactaaa gaggaagtgc tgcagaaagt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacct gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg caggtgca ggcgtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgta taccgggtgc gctggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctgcctcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgcgtgacgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gctgtagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccgt ttattcacca gtgcaaacg caccgggtc aaatttgag cgcgcagcaa 840
atgctgtgc tgctgcaggg cagccaactg atccgtgac agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgctgcg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaacg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 782

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 782

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```


145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Ser	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 783
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 783
atgatcattg cgagccagac ccaaaccttc accagcaaat ttccgcacac cgcgagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgt cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacgcttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgctaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg attcgtgacg agctggatgg tagccacgac 900
taccgtggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 784
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 784
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Ser	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355						360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435						440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 785

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 785

atgatcattg	cgagccagac	ccaaaccttc	accagcaaat	ttccgcacac	cgcgagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgctg	120
tatgggtgca	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagaaagt	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctgt	cgctggcgga	tgcttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggctgca	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggatccgcgg	tgatgaccgg	tattgctggc	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccaactg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccattg	cggacgggat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaat	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcacatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 786
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 786
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Phe Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Lys Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 788

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 788

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 789

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 789

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacggttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac cagcgtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 790

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 790

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450														

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ser				

<210> 791
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 791
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
 tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgtgacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcgtgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 792
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 792

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280							285		
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555							560
Ser	Ile														

<210> 793

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 793

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaacgc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 794

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 794

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 795

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 795

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagggtgt taactcgagc 180
tgcgagtggg tggcgcaagc gggtgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgagacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 796

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 796

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```


Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555
Ser	Ile																	

<210> 797

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 797

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg aagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgagacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 798

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 798

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Lys	Lys	
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser 185	Tyr	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Gln 285	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu 335	Ile	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr 430	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala 445	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545					550					555					560				
Ser	Ile																		

<210> 799

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 799

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gcaccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 800

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 800

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505						510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520							525	
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 801

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 801

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagcgtgt	taactcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctggttggg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	gtccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 802

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 802

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490						495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535					540							
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 803

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 803

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgct 120


```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg tcaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 804

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 804

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
					295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
					535						540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ser

<210> 805

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 805

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtgacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg tcaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 806

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 806

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295						300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390						395				400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 808
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 808
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Val Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 809

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 809

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 810

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 810

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 811

```
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagggtgt taactcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggt 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtgacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttgg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 812

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 812

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 813
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 813

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcg	120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tcagcgcgct	taacagcagc	180
tgcgagtggg	tggcgagcgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcggtaggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgcttcgtgc	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgctttg	cgaatttgg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcacatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgcttc	1320
ccgaccacag	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	tcaggcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 814
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 814

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 815

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 815

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgcaagc gggttgcgaag ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtgacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggc 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgct 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 816

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 816

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Val Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390						395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550						555					560	
Ser	Ile															

<210> 817

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 817

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgtgctg gaccgacaaa gaggaagtgc tgcagggtgt taactcgagc 180
tgcgagtggg tggcgaacgc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```



```

ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg cagggtgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacagtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaacgc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 818

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 818

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
50          55          60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145	150								155				160				
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555							

<210> 819
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 819
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgcttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgtg tcgagacctt cctgaacgag ggcgtgacct cgacgcttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatga tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gctgtagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgctg atccgtgac agctggatgg tagccacgac 900
taccgcgccg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcg aggatattac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 820
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 820
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 821

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 821

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgctg	120
tatgggtgca	aggcgctgct	gaccgacaaa	gaggaagtgc	tgcagggtgt	taactcgagc	180
tgcgagtggg	tggcgaacgc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacgggtcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	gtccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgctgctg	gcagtatacc	960
ggcccgattg	cggacgggat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcca	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagccgc	gcaccgtca	actgtatctg	gcgattaagg	aagtggttgg	tcaggcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 822
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 822
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Val Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggtttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 824

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 824

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```


Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 825

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 825

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgcaagc gggtgcaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcggg tggttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtgacctt cctgaacgcg ggctgacctc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtc caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgtgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 826

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 826

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
```

			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450														

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ser				

<210> 827
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 827
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
 tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcggg tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgtgacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
 agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcgtgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 828
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 828

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 829

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 829

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

<210> 830

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 830

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 831

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 831

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgcaagc gggtgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480

```



```

agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 832

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 832

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555
Ser	Ile																	

<210> 833

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 833

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagcgc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgagacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgaatgacgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 834

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 834

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn	Leu 100	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly 120	Met	Leu	Leu	Arg	Ala	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala	Leu 200	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn	Gly 255	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp	Arg 310	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
Met	Asp 370	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn 450	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545				550					555					560					
Ser	Ile																		

<210> 835

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 835

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagggtgt taactcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcaciaaagc ggggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggc 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg tcaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 836

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 836

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 837

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 837

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgaacgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgagacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccggtgc gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020

```

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtgggttg tcaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 838

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 838

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```


				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ser																

<210> 839

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 839

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 840

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 840

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 841

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 841

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgagacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcccgg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgcccgc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg tcaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 842

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 842

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5				10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile	
			20					25					30			
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr	
		35					40					45				
Thr	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	


```

agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 844
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 844
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Asp Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500				505						510		
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 845

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 845

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```



```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 846

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 846

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 847

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgctcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtgc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 848

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 848

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 849
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 849

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggcca	ggttgcgct	120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tcagcgtgt	taactcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tgctcgtgcg	360
ggtatgctgc	tgctgagcaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgcttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggtggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcacatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgcttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 850
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 850

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 851

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 851

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcggc 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg cagaagctgc cgctggcggg tggttcgtgcg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccc caccgggttc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg tcaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 852

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 852

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Gly Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```


Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280				285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ser															

<210> 853

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 853

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggc tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgca gcggtatccg tctggagctg 420
attcagcgta tcgagacctt cctgaacgcg ggcgtgacct cgacagtgtt cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg tcaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 854

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 854

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 855
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 855
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcaggggtg taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 856
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 856
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 857

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 857

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcggc	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgctg	120
tatgggtgca	aggcgctgct	gaccgacaaa	gaggaagtgc	tgcagggtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcaggggc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	gtccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcaccgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 858
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 858
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Gly Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Val Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaac cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgag 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 860

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 860

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Thr	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ser																		

<210> 861

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 861

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaacgc gggtgcgaag ggtgaaccga ttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtgacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtc caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 862

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 862

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

100						105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135					140				
Val	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				

530	535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val	
545	550	555
Ser Ile		

<210> 863
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 863

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgacgcgtgt	taactcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcggtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgagacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tggtgctgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tggtgaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	tcaggcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 864
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 864

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555							560
Ser	Ile														

<210> 865

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 865

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
tatggtgcca aggcgctgct gaccacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgcaagc gggtgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgagacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttgg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg tcaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 866

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 866

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```


290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Gln Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 867

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 867

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgagacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 868

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 868

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 869

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 869

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagggtgt taactcgagc 180
tgcgagtggg tggcgcaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgtgacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtggttgg tcaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 870

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 870

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn	Leu 100	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly	Lys	Lys	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly 120	Met	Leu	Leu	Arg	Ala	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Val 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala	Leu 200	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn	Gly 255	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp	Arg 310	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
Met	Asp 370	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn 450	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545					550					555					560				
Ser	Ser																		

<210> 871

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 871

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgagacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggc 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg tcaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 872

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 872

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Gln	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 873

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 873

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg gtccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020

```



```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 874

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 874

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Val	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490						495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535					540							
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 875

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 875

atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg ttagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatattac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 876

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 876

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Val	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 877

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 877

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgctg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgagg aggatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 878

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 878

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt                                                                    1686

```

```

<210> 880
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 880
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```


Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 881

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 881

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgctg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgacga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgctggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgagg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 882
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 882
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 883

```
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgagg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 884

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 884

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 885
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 885

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	agttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccactaaa	gaggaagtgc	tcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	cagtatatgt	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caagggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 886
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 886

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 887

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 887

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcgc ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```



```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 888

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 888

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390						395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550					555						560	
Ser	Ile															

<210> 889

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 889

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgct 120
tatggtgcga aggcgtgct gaccactaaa gaggaagtgc tgcagcgct taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga tttacggcgt taccactgg 240
ttcgggtggc tggcgaact ggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg cacgggtgca gcgggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacagtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcaggggc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaaagc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcggtggcg cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 890

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 890

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 891
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 891
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgcttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgacggg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcggg aggatattac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 892
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 892
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 893

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 893

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccca	agttgcgcgt	120
tatgggtgca	aggcgcgtct	gaccactaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacgggtcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgaggttga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	cagtatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagctccg	1560
gataaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	ctcgggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 894
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 894
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 896

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 896

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 897

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 897

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacggttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta ca taccgggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 898

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 898

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 899
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 899
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
 tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
 tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcgtgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 900
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 900

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555							560
Ser	Ile														

<210> 901

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 901

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataaccg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```



```

ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg ttagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 902

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 902

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Val Ala Pro Asp Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 903

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 903

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 904

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 904

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245				250						255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 905

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 905

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatggtgcga aggcgcgtct gacctataa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagcgc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 906

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 906

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn	Leu 100	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly 120	Met	Leu	Leu	Arg	Ala	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala	Leu 200	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn	Gly 255	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Glu 305	Pro	Ile	Gln	Asp	Arg 310	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn 350	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser 365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp 385	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr 430	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala 445	Glu	Gln	Phe	Asn 450	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg 465	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	


```
<211> 562
<212> PRT
<213> Artificial Sequence
```

 $\langle 220 \rangle$

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 908

Met 1	Ile	Ile	Ala	Ser 5	Gln	Thr	Gln	Thr	Phe 10	Thr	Ser	Lys	Ser	Pro 15	His
Thr	Ala	Ser	Asp 20	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
Asn	Glu	Val	Ala	Gln	Val	Ala	Arg 40	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
Thr	Lys 50	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly	Gln	Lys
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 909

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 909

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	cgttgcgcgt	120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tggtcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 910

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 910

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490						495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu		
	530				535					540							
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 911

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 911

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120

```

tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggatga cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaat tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 912

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 912

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
					295						300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
					535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 913

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 913

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcgaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 914

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 914

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 916
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 916
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Glu Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 917

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 917

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaacccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tcaagaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgagg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 918

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 918

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 919

```
atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgcttcgtgcg 360
ggtagtgcgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag tactatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 920

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 920

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 921
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 921

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	cgttgcgcgt	120
tatggtgcga	aggcgtgct	gaccactaaa	gaggaagtgc	tcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	cagtatatgt	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgca	1620
gccatcgcg	aggatatcac	caagggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 922
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 922

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 923

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 923

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gacctataa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgct taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgagg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 924

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 924

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390						395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550					555						560	
Ser	Ile															

<210> 925

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 925

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacagtgtt cgaatttgggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttgggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatattcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 926

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 926

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550												

<210> 927
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 927
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaacctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatcacac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 928
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 928
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435				440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 929

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 929

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccca	agttgcgcgt	120
tatgggtgca	aggcgcgtct	gaccactaaa	gaggaagtgc	tgcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacgggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgcttgc	gcagtatacc	960
ggcccgattg	cggacgggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttgc	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	gtagcattga	aatcttccag	cagtatatatt	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgca	1620
ctgatcgcg	aggatatcac	caagggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 930
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 930
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 932

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 932

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 933

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 933

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cccccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 934

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 934

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 935
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 935
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
 tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctg cgacgcttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
 tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
 gccatcgcgg aggatattac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 936
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 936

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 937

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 937

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgccgct 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag tactatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 938

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 938

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Tyr Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Ala Ile Ala Glu				
	530		535	540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 939

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 939

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatgggtgca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 940

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 940

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	530	535	540
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555
Ser	Ile																	

<210> 941

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 941

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gacctataa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagcgc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc ggggtgcggc caaagctgc cgctggcgga tgttcgtgcg 360
ggtagctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgacggg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg tgtagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 942

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 942

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50					55					60				
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn	Asn	Leu 100	Met	Leu	Tyr	His	Lys 105	Ala	Gly	Ala	Gly	Gln	Lys
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser	Gly 165	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly	Ala 245	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly 255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp	Arg 310	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp	Gly 325	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile 335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Val	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu				
	530					535						540							
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545					550					555					560				
Ser	Ile																		

<210> 943

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 943

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgccgct 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcgagg ggttgcggaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgcgtgacgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag tactatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 944

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 944

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455				460					
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 945

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 945

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccgc	cgttgcgcgt	120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgcg	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tggtcgtgcg	360
ggatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccgggtg	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtgggttg taaacctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 946

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 946

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490						495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530			535						540							
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 947

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 947

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120

```

tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggatga cctgaccccg ctggcgatga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 948

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 948

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
					295						300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
					535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 949

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 949

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 950

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 950

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

<210> 952
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 952
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 953

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 953

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgct 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggagaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgacga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtggttgg taaagctccg 1560
gataaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgagg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 954
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 954
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 955

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgcttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgccgaaatc gcgaagcaaa tcgaggttga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatatg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 956

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 956

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 957
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 957

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	agttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccactaaa	gaggaagtgc	tcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgccgaaatc	gcgaagcaaa	tcgaggttga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgacccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatcttccag	cagtatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattcgc	1620
ctgatcgcgg	aggatatcac	caagggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 958
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 958

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 959

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 959

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 960

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 960

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505					510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 961

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 961

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgct 120
tatggtgcga aggcgtgct gaccactaaa gaggaagtgc tgcagcgct taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga tttacggcgt taccactgg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg cagggtgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacagtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcaggggc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccgggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaacgc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 962

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 962

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 963
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 963
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgc atcacaagc gggtgcgggc caaagctgc cgctggcgga tgcttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgag ggcgtgacct cgacgcttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gctgtagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgctg atccgtgac agctggatgg tagccacgac 900
taccgcgccg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgaggttga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatat cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcg aggatattac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 964
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 964
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 965

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 965

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccgc	cgttgcgcgt	120
tatgggtgca	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgcg	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacgggtgcg	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttgg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagagccgat	ccaagatcgt	tacagcctgc	gttgcttgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcca	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	cagtatatattg	cgatcgcgct	gatgtttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcaccgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattcgc	1620
ctgatcgcg	aggatatcac	ctcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 966
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 966
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Glu Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 968

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 968

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 969

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 969

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgctca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 970

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 970

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

100						105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				

530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 971
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 971
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgcgt 120
 tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgctgt atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgacctg cgacgtttg cgaatttggg 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 972
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 972

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 973

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 973

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgacccgtc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 974

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 974

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Arg Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 975

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 975

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg tgtagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 976

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 976

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510
Lys	Glu	Val	Val	Gly	Val	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	530	535	540
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555
Ser	Ile																	

<210> 977

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 977

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagcgc ggttgcggaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgaggttga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 978

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 978

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser 185	Tyr	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln 280	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Val 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545				550					555						560				
Ser	Ile																		

<210> 979

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 979

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgccgct 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcgaggc gggtgcaagc ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggttatcac ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggc 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tcaagaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattgggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 980

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 980

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Gln	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 981

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 981

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	cgttgcgcgt	120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tggtcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgtag	cgcgagcaga	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 982

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 982

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490						495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 983

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 983

atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgaggttga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 984

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 984

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
					535						540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 985

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 985

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca agttgcgcgt 120
tatgggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcga cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatcg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 986

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 986

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390						395				400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 988
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 988
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 989

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 989

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgctg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gcacccgtca actgtatctg gcgattaagg aagtggttgg taaacctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgagg aggatatac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 990

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 990

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 991

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgcttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtgc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tcaagaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctactgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgagg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 992

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 992

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Gln	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 993
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 993

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	agttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccactaaa	gaggaagtgc	tcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	cagtatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaagctccg	1560
gataaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgca	1620
ctgatcgcg	aggatatcac	ctcgggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 994
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 994

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 995

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 995

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 996

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 996

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 997

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 997

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgctgt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcaaa cagccacctg cacgggtgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gctgtagcc tgggtgcaaa tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccgt ttattcacca gtgcaaaccc caccgggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgccg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaacgc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgag 1560
agcaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcg aggatatcac ctcggtggcg cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 998

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 998

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Gln	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 999
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 999
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatat cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg tgtagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcg aggatatcac ctcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1000
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1000
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr	
		35					40					45				
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115				120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340				345						350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Val	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 1001

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1001

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccgc	cgttgcgcgt	120
tatgggtgca	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgcg	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacgggtgcg	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttgg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccggg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccattg	cggacgggat	tgccgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaat	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaagg	tctgcagatt	1260
accggttaac	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	cagtatatatt	cgatcgcgct	gatgtttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcaccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgca	1620
ctgatcgcg	aggatatcac	caagggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1002
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1002
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Glu Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgca actgtatctg gcgattaagg aagtggttgg taaacctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1004
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1004
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 1005

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1005

```
atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctg gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1006

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1006

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450														

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 1007
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1007
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
 tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctg cgacgcttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
 atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcgtgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 1008
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1008

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1009

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1009

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1010
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1010
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 1011

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1011

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1012
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1012
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1013

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1013

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gacctataaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagcgc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gacccgtca actgtatctg gcgattaagg aagtggttgg tgtagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1014

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1014

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```


	50				55				60							
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn	Leu 100	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly 120	Met	Leu	Leu	Arg	Ala	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala	Leu 200	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn	Gly 255	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp	Arg 310	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
Met	Asp 370	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn 450	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Val	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545					550					555					560				
Ser	Ile																		

<210> 1015

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1015

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgccgct 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcgaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg tgtagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1016

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1016

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470					475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505						510		
Lys	Glu	Val	Val	Gly	Val	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ile														

<210> 1017

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1017

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccca	agttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccactaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tggtcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaga	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag cagtatttg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1018

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1018

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 1019

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1019

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1020
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1020
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
					295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
					535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1021
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1021
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatgggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1022
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1022
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Asn	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
			85						90					95			
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 1024
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 1024
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Glu Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1025

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1025

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaacctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1026
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1026
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1027

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtgc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag cagtatatatg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
gataaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgagg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1028

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1028

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```


Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1029
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1029

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	cgttgcgcgt	120
tatggtgcga	aggcgtgct	gaccactaaa	gaggaagtgc	tcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgcgt	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacgggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgacccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	caagggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1030
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1030

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1031

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1031

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgagg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1032
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1032
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550					555						560	
Ser	Ile															

<210> 1033

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1033

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgct 120
tatggtgcga aggcgtgct gaccactaaa gaggaagtgc tgcagcgct taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga ttacggcgt taccactggt 240
ttcgggtggca tggcgaacct ggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgctgt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacagtgtg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag tactatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1034
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1034
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550												

<210> 1035
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1035
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgc atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgctg tgatgaccgg tattgcggcg aactgcgttc atgatgctga gaacctgctg 720
gctgtagctg tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgctg atccgtgac agctggatgg tagccacgac 900
taccgctggc aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccgt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacctgtc gtagcattga aatcttccag caatatattg cgatcgctg gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgctg aggatattac ctcggtgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1036
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1036
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr	
		35					40					45				
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115				120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340				345						350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 1037

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1037

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	cgttgcgcgt	120
tatgggtgca	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgcg	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatg	atcacaagc	gggtgcgggc	caaagctgc	cgctggcgga	tgctcgtgcg	360
ggatgctgc	tgcgtgcgaa	cagccacctg	cacgggtgcg	gcggatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacg	ggcgtgacc	cgacgcttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgacccg	ctggcgta	tcaccggtg	gctggttggt	540
ctgaacgaca	gttataacgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggatccgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagagccgat	ccaagatcgt	tacagcctgc	gttgctgctg	gcagtatacc	960
ggcccgattg	cggacggtat	tgccgaaatc	gcgaagcaaa	tcgaggttga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcca	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgcttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	cagtatat	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagccgc	gcaccgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	ctcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1038
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1038
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Glu Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1040
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1040
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 1041

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1041

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacggttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca taccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1042

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1042

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```


			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450														

530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 1043
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1043
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgcgt 120
 tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgctgt atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctg cgacgcttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
 ctgatcgcgg aggatattac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 1044
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1044

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555							560
Ser	Ile														

<210> 1045

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1045

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1046
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1046
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Asp Lys Asp Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Arg Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 1047

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1047

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatgggtgca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1048
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1048
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1049

<211> 1686

<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1049

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagcgc ggttgcggaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgaggttga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1050

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1050

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser 185	Tyr	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu 295	Leu	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Val 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1052

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455				460					
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1053

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1053

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccggtgc gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020

```

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1054
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1054
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 1055

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1055

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tcaagaaatc gcgaagcaaa tcgaggttga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg ttagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1056
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1056
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```


His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Gln	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Val	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1057
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1057
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca agttgcgcgt 120
tatgggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcga cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatattac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1058
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1058
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195					200						205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390						395				400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

tcgaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt                                     1686

```

```

<210> 1060
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 1060
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Glu Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Val	Pro	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1061

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1061

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggcca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgacga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag cagtatatatg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtggttgg taaagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1062
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1062
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1063

```
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtagtctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1064

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1064

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1065
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1065

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	cgttgcgcgt	120
tatggtgcga	aggcgtgct	gaccactaaa	gaggaagtgc	tcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcgggtga	cctgaccccg	ctggcgtaca	tcaccgggtgc	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacgggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	tactatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	ctcgggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1066
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1066

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1067

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1067

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1068
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1068
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550					555						560	
Ser	Ile															

<210> 1069

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1069

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgct 120
tatggtgcga aggcgtgct gaccactaaa gaggaagtgc tgcagcgct taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1070

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1070

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```


145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1071
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1071
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggcgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatattac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1072
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1072
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys 35	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
Thr 50	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
Ala 65	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
Glu 305	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 1073

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1073

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccgc	cgttgcgcgt	120
tatgggtgca	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgcg	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatg	cgct	atcacaagc	gggtgcgggc	caaaagctgc	cgctggcgga	360
ggatg	ctgc	tgcgtgcgaa	cagccacctg	cacgggtgcga	gcggtatccg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttgg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggataccg	cggtg	tgtatgacgg	tattgcggcg	aactgcgttc	atgatgcgca	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgcttgc	gcagtatacc	960
ggcccgattg	cggacgggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttgc	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcca	gtag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	cagtatatattg	cgatcgcgct	gatgtttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaagctccg	1560
gataaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgca	1620
ctgatcgcg	aggatatcac	caagggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1074
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1074
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1076
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1076
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 1077

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1077

```
atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1078

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1078

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450														

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 1079
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1079
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
 tatggtgcca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgacctg cgacgcttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgatga tcaccggtgc gctgggtggg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag cagtatatgg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 1080
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1080

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280						285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390							395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555							560
Ser	Ile														

<210> 1081

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1081

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgcgt 120
tatggtgcca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggatggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg ttagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1082
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1082
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Val Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Ala Ile Ala Glu				
	530		535	540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 1083

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1083

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1084
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1084
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```


Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245				250						255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260				265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370				375						380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1085

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1085

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gacctataa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagcgc ggttgcgaa ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggctc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1086

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1086

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50					55					60				
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg 125	Ala	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro 270	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln 285	Gly	Ser
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335
Glu	Ile	Asn 340	Ser	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu	Thr 390	Met	Pro	Glu	Phe	Asn 395	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415
Gly	Leu	Gln	Ile	Thr 420	Gly	Asn	Ser	Ile	Met 425	Pro	Leu	Leu	Thr 430	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro 440	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln 470	Tyr	Ile	Ala	Ile	Ala 475	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545				550					555						560				
Ser	Ile																		

<210> 1087

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1087

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgccgct 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcgagg ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1088

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1088

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470					475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ile														

<210> 1089

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1089

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccgc	cgttgcgcgt	120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgcg	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tggtcgtg	360
ggatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag cagtatttg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 1090
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1090
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 1091

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1091

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cggttgcgct 120


```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgctg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1092
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1092
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1093
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1093
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatgggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1094
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1094
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Asn	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Lys	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
			85						90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		

tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
 ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
 agcatt 1686

<210> 1096
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1096
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535				540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1097

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1097

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca agttgcgcgt 120
tatggtgcca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggagaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgagg aggatatac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 1098
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1098
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1099

```
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgagg aggatatcac ctcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1100

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1100

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1101
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1101

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccgc	cgttgcgcgt	120
tatggtgcga	aggcgtgct	gaccactaaa	gaggaagtgc	tgacgcgcgt	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgcttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggtggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcgggc	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacgggat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgacccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatcttccag	cagtatatgt	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagctccg	1560
tcgaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1102
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1102

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1103

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1103

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgcgtgagcc tgcgtgagcc aactgcgttc atgatgcgca gaacctgctg 720
gtagctgagc tgggtgagca tgcgtgagcc ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgct 1620
ctgatcgcgg aggatattcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1104
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1104
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350
 Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser
 355 360 365
 Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp
 370 375 380
 Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro
 385 390 395 400
 Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys
 405 410 415
 Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr
 420 425 430
 Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn
 435 440 445
 Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg
 450 455 460
 Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly
 465 470 475 480
 Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp
 485 490 495
 Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile
 500 505 510
 Lys Glu Val Val Gly Lys Ala Pro Asp Lys Glu Arg Pro Tyr Ile Trp
 515 520 525
 Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu
 530 535 540
 Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ile

<210> 1105

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1105

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgct 120
 tatggtgcga aggcgtgct gaccactaaa gaggaagtgc tgcagcgct taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggc 240
 ttcggtggca tggcgaacct gggtatcacc ccggaccagg cgaaggagct gcagaataac 300


```

ctgatgcgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg cacgggtgca gcgggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gctgtagacc tgggtgcaaa tgcgctggcg ctgcaggggc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaacgc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
gataaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1106

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1106

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1107
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1107
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacgcttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag cagtatatcg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1108
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1108
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr	
		35					40					45				
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115				120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 1109

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1109

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	cgttgcgcgt	120
tatgggtgca	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgcg	taacagcagc	180
tgcgagtggg	tggcgagggc	gggtgcgaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatgctgc	tgcgtgcgaa	cagccacctg	cacgggtgcga	gcggatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgcttg	cgaatttgg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggatccgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgcttgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgccgaaatc	gcgaagcaaa	tcgagggtga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaat	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcaccgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	ctcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1110
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1110
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1112
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1112
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```


Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 1113

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1113

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1114

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1114

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 1115
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1115
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
 tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgctgt atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
 gataaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
 ctgatcgcgg aggatattac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 1116
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1116

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1117

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1117

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatgggtgca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggatggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg tgtagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

<210> 1118
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1118
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Glu Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Val Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Arg Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 1119

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1119

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatgggtgca aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480

```



```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcaccgctca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1120
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1120
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1121

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1121

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gacctataa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagcgc ggttgcgaa ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaagc ggggtgcggc caaagctgc cgctggcgga tgttcgtgcg 360
ggtagctgct tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg ttagtaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1122

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1122

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50					55					60				
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg 125	Ala	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro 270	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln 285	Gly	Ser
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Glu 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Val 335
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu	Thr 390	Met	Pro	Glu	Phe	Asn 395	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys
Gly	Leu	Gln	Ile	Thr 420	Gly	Asn	Ser	Ile	Met 425	Pro	Leu	Leu	Thr 430	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro 440	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln 470	Tyr	Ile	Ala	Ile	Ala 475	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1124

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1125

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1125

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	agttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccactaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tggtcgtgctg	360
ggatgctgct	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccgct	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag cagtatttg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1126
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1126
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```


				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 1127

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1127

atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgct 120

```

tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggatga cctgaccccg ctggcgatga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaat tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1128
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1128
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1129
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1129
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgct 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1130
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1130
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55				60							
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
			85					90						95			
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195					200						205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		

tcgaaagatc gtccttatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
 ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
 agcatt 1686

<210> 1132
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1132
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Glu Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Val	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1133
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1133
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggcca agttgcgcgt 120
 tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgctgt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660


```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgagg aggatatcac ctgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1134
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1134
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1135

```
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgctcgctgc 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtgc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgagg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1136

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1136

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1137
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1137

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcg	120
tatggtgcga	aggcgtgct	gaccactaaa	gaggaagtgc	tcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcggaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttgg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcgtaca	tcaccgggtgc	gctgggttgg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgtggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacgggtat	tgccgaaatc	gcgaagcaaa	tcgaggttga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	cagtatatattg	cgatcgcgct	gatgtttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaacctccg	1560
tcgaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgca	1620
ctgatcgcgg	aggatatcac	caagggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1138
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1138

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1139

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1139

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag tactatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg tgtacctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1140
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1140
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```


Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390						395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Val	Pro	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550						555					560	
Ser	Ile															

<210> 1141

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1141

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca ggttgcgct 120
tatggtgcga aggcgtgct gaccactaaa gaggaagtgc tgcagcgct taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcgggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacagtttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatat cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaacctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1142

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1142

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550												

<210> 1143
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1143
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag tactatatg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcg aggatatcac ctcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1144
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1144
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435				440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 1145

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1145

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccgc	cgttgcgcgt	120
tatgggtgca	aggcgcgtct	gaccactaaa	gaggaagtgc	tgcagcgcg	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatg	atcacaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgcttcgtgc	360
ggatgctgc	tgcgtgcgaa	cagccacctg	cacgggtgcga	gcggatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgcttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggatccgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcaggggc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagagccgat	ccaagatcgt	tacagcctgc	gttgcttgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgccgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaat	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	cagtatatatt	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcaccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagctccg	1560
tcgaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	ctcgggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1146
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1146
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Glu Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1148
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1148
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 1149

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1149

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatgggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcg aggatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1150

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1150

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450														

530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 1151
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1151
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgcgt 120
 tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgcttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgcctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 1152
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1152

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1153

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1153

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcgga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1154
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1154
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```


290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		560
Ser Ile				

<210> 1155

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1155

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg taaagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1156
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1156
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1157

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1157

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccca agttgcgcgt 120
tatggtgcga aggcgctgct gacctataaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagcgc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcaciaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtagctgct tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgacggg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgaggttga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcaccgtca actgtatctg gcgattaagg aagtgggttg tgtagctccg 1560
gataaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgctg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1158

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1158

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50					55					60				
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn	Asn	Leu 100	Met	Leu	Tyr	His 105	Lys	Ala	Gly	Ala	Gly	Gln	Lys
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly 120	Met	Leu	Leu	Arg	Ala	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala	Leu 200	Lys	Leu	Leu	Gly	Leu 205	Glu	Pro	Leu
Glu	Leu 210	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn	Gly 255
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp	Arg 310	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Val 335
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
Met	Asp 370	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln	Asn 450	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Val	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545					550					555					560				
Ser	Ile																		

<210> 1159

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1159

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgccgct 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcgagg ggttgcggaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaact ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagggtga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1160

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1160

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1161

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1161

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccca	agttgcgcgt	120
tatggtgcga	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgc	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tggtcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgccgaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020


```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1162
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1162
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490						495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu		
	530				535					540							
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 1163

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1163

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120

```

tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggatga cctgaccccg ctggcgatga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1164
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1164
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
					295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
					535						540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1165

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1165

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaacg aggtggccgc cgttgcgctg 120
tatgggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1166

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1166

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195					200						205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagaac gtccttatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 1168
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 1168
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```


Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1169

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1169

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagctccg 1560
gataaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgagg aggatatcac ctggggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1170
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1170
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1171

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca agttgcgcgt 120
tatggtgcga aggcgcgtct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgcttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgccgaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag cagtatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
tcgaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
gccatcgagg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1172

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1172

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Ala	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1173
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1173

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaacg	aggtggccca	agttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccactaaa	gaggaagtgc	tcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacagccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacgggat	tgcggaaatc	gcgaagcaaa	tcgaggttga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	tactatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaacctccg	1560
tcgaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgca	1620
ctgatcgcgg	aggatatcac	caagggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1174
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1174

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Pro	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1175

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1175

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc cgttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacagccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```



```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac ctcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1176
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1176
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405				410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470				475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485				490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ile																

<210> 1177

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1177

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg caggtgca ggcgtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgta taccgggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccgt ttattcacca gtgcaaaccc caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgctgcg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1178

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1178

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1179
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1179
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacggttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1180
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1180
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 1181

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1181

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgctg	120
tatgggtgca	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctgc	cgctggcgga	tgcttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccaactg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcttgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagatcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccaagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
tcgaaagatc	gtccgtatat	ctggaacgac	gatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcgacggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagc						1686

<210> 1182
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1182
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1184
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1184
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 1185

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1185

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgta ca taccgggtgc gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgcctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1186

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1186

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450														

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 1187
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1187
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgacctg cgacgtttg cgaatttggg 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgtctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 1188
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1188

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1189

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1189

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggttgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc cgggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggc cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```


290		295		300	
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr					
305		310		315	320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile					
	325		330		335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn					
	340		345		350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser					
	355		360		365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp					
	370		375		380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro					
385		390		395	400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys					
	405		410		415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr					
	420		425		430
Gly Asn Ser Val Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn					
	435		440		445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg					
	450		455		460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ile					

<210> 1191

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1191

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1192
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1192
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1193

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1193

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagcgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1194

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1194

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu 295	Leu	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn 340	Ser	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile	Met 425	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro 440	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545					550					555					560				
Ser	Ile																		

<210> 1195

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1195

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattgggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1196

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1196

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1197

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1197

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgct taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020

```

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1198
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1198
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325				330						335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420				425							430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 1199

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1199

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagcgcgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1200
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1200
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
					295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
					535						540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1201
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1201
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1202
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1202
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgagg aggatatacac cagcagcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 1204
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 1204
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Ser	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1205

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1205

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taactcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgtagcgagg tattgaggcg aactgagttt atgtagcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt

```

<210> 1206
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1206
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1207

```
atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcggt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgcggt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcggt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1208

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1208

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	
		100						105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1209
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1209

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggcca	ggttgcgct	120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tcagcgct	taacagcagc	180
tgcgagtggg	tggcgaggc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgcttcgtgcg	360
ggtatgctgc	tgctgagaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctgggtggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgctggc	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccaactg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcgacggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1210
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1210

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1211

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1211

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatc                                     1686

```

<210> 1212
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1212
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390						395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550						555					560	
Ser	Ile															

<210> 1213

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1213

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgtgctg gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacagtgtt cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1214
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1214
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
				275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
				500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
				515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
				530					535					540			
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550												

<210> 1215
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1215
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgacga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacgcttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgacggg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gagctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcgagg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatattac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1216
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1216
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1217

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1217

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcggt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgctctgctg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgacccc cgacgctttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgag tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gtagctgagc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cgagcgagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
tcgaaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgct 1620
ctgatcgagg aggatattac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagc

```


<210> 1218
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1218
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgag 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1220
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1220
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 1221

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1221

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta ca taccgggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatc 1686
```

<210> 1222

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1222

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530	535	540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val	
545	550	555
Ser Ile		

<210> 1223
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1223
 atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
 tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcgac 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 1224
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1224

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1225

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1225

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
tatgggtgca aggcgcgtct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc cgggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1226
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1226
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asp Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 1227

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1227

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1228
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1228
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245				250						255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370				375						380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1229

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1229

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagcgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1230

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1230

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys	
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu 295	Leu	Asp	Gly	Ser	His 300	Asp	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn 340	Ser	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile	Met 425	Pro	Leu	Leu	Thr	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro 440	Thr	His	Ala	Glu	Gln	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545				550					555						560				
Ser	Ile																		

<210> 1231
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1231

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgtctgt	gaccgacaaa	gaggaagtgc	tgacgcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgtctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccag	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gtagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accgtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcaccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcgacggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1232

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1232

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1233

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1233

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacct	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tggtcgtgctg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgtctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
tcgaaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatc
1686

```

<210> 1234
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1234
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360					365						
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375				380								
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425					430					
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455				460								
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470				475						480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485				490					495					
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 1235
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1235
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggatga cctgaccccg ctggcgatga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaat tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1236
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1236
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1237
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1237
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1238
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1238
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390						395				400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgagg aggatatacac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagc 1686

```

```

<210> 1240
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 1240
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1241

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1241

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgacga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgctggcg aagaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1242
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1242
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1243

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgcgtct gaccacaaa gaggaagtgc tgcagcgcgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagc 1686
```

<210> 1244

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1244

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1245
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1245

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggcca	ggttgcgct	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tcagcgct	taacagcagc	180
tgcgagtggg	tggcgaggc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgctcgctgcg	360
ggtatgctgc	tgctgagaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgcttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctgggtggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgctggc	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgtctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgaggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgcttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
gataaagatc	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1246
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1246

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1247

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1247

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 1248
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1248
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345						350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390						395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550					555						560	
Ser	Ile															

<210> 1249

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1249

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca ggttgcgct 120
tatggtgcga aggcgtgct gaccacaaa gaggaagtgc tgcagcgct taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga ttacggcgt taccactggt 240
ttcgggtggc tggcgaact ggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg cagggtgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacagtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggtttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcaggggc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaacgc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1250

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1250

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145									150									155									160							
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly																			
																165									170									175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu																			
																180									185									190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu																			
																195									200									205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val																			
																210									215									220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu																			
																225									230									235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly																			
																245									250									255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro																			
																260									265									270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser																			
																275									280									285
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu																			
																290									295									300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr																			
																305									310									315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile																			
																325									330									335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn																			
																340									345									350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser																			
																355									360									365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp																			
																370									375									380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro																			
																385									390									395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys																			
																405									410									415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr																			
																420									425									430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn																			
																435									440									445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg																			
																450									455									460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly																			
																465									470									475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp																			
																485									490									495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile																			
																500									505									510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp																			
																515									520									525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu																			
																530									535									540
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val																			
																545									550									

<210> 1251
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1251
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacgcttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatc 1686

<210> 1252
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1252
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr	
		35					40					45				
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115				120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1253

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1253

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgctctgctg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgag tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gtagctgagc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgtgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
gataaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatattac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagc
1686

```

<210> 1254
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1254
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1256
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1256
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 1257

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1257

```
atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta ca taccgggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1258

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1258

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
```

100						105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val			
545	550	555	560	
Ser Ile				

<210> 1259
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1259
 atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
 tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaagc gggtgctggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccaactg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
 agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcgtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 1260
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1260

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1261

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1261

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggttgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1262
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1262
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Asp Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 1263

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1263

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1264
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1264
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1265

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1265

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgagcgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgcgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1266

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1266

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Lys	Lys	
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser 185	Tyr	Thr	Val	Asp	Phe	Asn 190	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu	Leu 210	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Gln 285	Gly	Ser	
Gln	Leu 290	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu	
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp	
Val 385	Gln	Ile	Ala	Leu	Leu	Thr 390	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr 430	Phe	Tyr	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu	Gln 445	Phe	Asn	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln 470	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545				550					555						560				
Ser	Ile																		

<210> 1267
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1267

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggcca	ggttgcgcgt	120
tatggtgcga	aggcgtctgt	gaccgacaaa	gaggaagtgc	tgacgcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccaactg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccag	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gtagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcaccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
gataaagagc	gtccgtatat	ctggaacgac	gatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1268

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1268

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1269

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1269

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacct gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020

```

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagagc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1270

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1270

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245				250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310					315						320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390					395						400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440				445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455				460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470				475						480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485				490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500				505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530				535					540						
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550				555						560		
Ser	Ile															

<210> 1271

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1271

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgccc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1272
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1272
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1273
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1273
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgca aggcgcgtct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1274
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1274
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 1276
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 1276
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1277

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1277

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg ttgtagcgagg tattgtagggc aactgtagttt atgtagcgca gaacctgtagt 720
gtagctgagcc tgggtgtagca tgcgctggcg ctgtagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgtaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgtaggg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtag tgcggaaatc gcgaagcaaa tcgaggtagc aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgctgt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgcccgg agtttaacaa cggctgtagc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgtagc gatgtttgg 1440
gtgcaaagcg ttgacctgag taccaagaaa attgcaagc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtggtagg taaagcgcc 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgag 1620
ctgtagcgag aggatatac cagcgtaggg cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagc

```

<210> 1278

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1278

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1279

```
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcg 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgcg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcggt taccactgg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgcttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttgg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagc 1686
```

<210> 1280

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1280

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1281
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1281

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggcca	ggttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccacaaa	gaggaagtgc	tcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggatga	cctgaccccg	ctggcgtaca	tcaccggtgc	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgcgt	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgtctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg	1560
gataaagagc	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcgacggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatc						1686

<210> 1282
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1282

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1283

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1283

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 1284
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1284
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280				285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1285

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1285

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcaaa cagccacctg cacgggtgcga gcgggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggtttgg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gctgtagacc tgggtgcaaa tgcgctggcg ctgcaggggc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaacgc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1286

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1286

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145									150									155									160							
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly																			
																165									170									175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu																			
																180									185									190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu																			
																195									200									205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val																			
																210									215									220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu																			
																225									230									235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly																			
																245									250									255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro																			
																260									265									270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser																			
																275									280									285
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu																			
																290									295									300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr																			
																305									310									315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val																			
																325									330									335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn																			
																340									345									350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser																			
																355									360									365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp																			
																370									375									380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro																			
																385									390									395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys																			
																405									410									415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr																			
																420									425									430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn																			
																435									440									445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg																			
																450									455									460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly																			
																465									470									475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp																			
																485									490									495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile																			
																500									505									510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp																			
																515									520									525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu																			
																530									535									540
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val																			
																545									5									

<210> 1287
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1287
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacgcttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1288
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1288
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
	35						40					45					
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435				440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 1289

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1289

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgaattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgtgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
gataaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatattac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagc

```

<210> 1290
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1290
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggtttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
tcgaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1292
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1292
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 1293

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1293

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1294

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1294

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

		100				105				110					
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120				125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
		130				135				140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145			150				155				160				
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
		165				170				175					
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180				185				190					
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195				200				205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215				220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225			230				235				240				
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
		245				250				255					
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260				265				270					
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280				285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295				300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305			310				315				320				
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
		325				330				335					
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340				345				350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355				360				365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375				380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385			390				395				400				
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
		405				410				415					
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420				425				430					
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440				445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455				460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465			470				475				480				
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
		485				490				495					
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500				505				510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520				525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 1295
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1295
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
 tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcgac 180
 tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgctggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgcttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccgtctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
 gataaagagc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagc 1686

<210> 1296
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1296

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1297

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1297

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggttgcgct 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggttgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc cgggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatc

```

<210> 1298
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1298
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 1299

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1299

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgaggatatacac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1300
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1300
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245					250						255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
		260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345						350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355						360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370				375						380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420					425						430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1301

<211> 1686

<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1301

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaggg gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg aaaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgaatgacgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
tcgaaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1302
<211> 562
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1302

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
```


	50					55					60				
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Lys	Lys
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser 185	Tyr	Thr	Val	Asp	Phe	Asn 190	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln 280	Met	Leu	Glu	Leu	Leu	Gln 285	Gly	Ser
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu 335	Ile
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr 430	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu	Gln 445	Phe	Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1304

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
	115					120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325						330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1305

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1305

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020

```

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatc
1686

```

<210> 1306

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1306

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325				330						335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420				425							430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505							510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 1307

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1307

atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1308
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1308
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1309
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1309
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1310
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1310
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr		
		35					40					45					
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340						345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		

agcaaagaac gtccttatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
 agcatt 1686

<210> 1312
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1312
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1313
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1313
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggcca ggttgcgcgt 120
 tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

ggtagcgagg tgtagcgagg tattgaggcg aactgagttc atgtagcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatac cagcggtagc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatc 1686

```

<210> 1314
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1314
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1315

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtgc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
tcgaaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattcgc 1620
ctgatcgagg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1316

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1316

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```


Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100						105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1317
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1317

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggcca	ggttgcgct	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgacgcgcgt	taacgcgagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtaggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccaactg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg	1560
agcaaagagc	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	cagcggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1318
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1318

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1319

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1319

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgaattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt
1686

```

<210> 1320
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1320
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280				285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1321

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1321

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca ggttgcgct 120
tatggtgcga aggcgcgtct gaccacaaa gaggaagtgc tgcagcgct taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaactt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcgggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1322

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1322

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```

145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1323
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1323
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacggttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
gataaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattcgc 1620
ctgatcgcg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1324
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1324
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340				345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ile														

<210> 1325

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1325

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgctg	120
tatgggtgca	aggcgctgct	gaccactaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctgc	cgctggcgga	tgcttcgtgcg	360
ggatatgctg	tgctgtcgaa	cagccacctg	cacgggtcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacagtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccgcctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcttgcc	gcagtatacc	960
ggcccgaattg	cggacgggat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaac	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcaccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcgacggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1326
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1326
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1328
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1328
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ile																		

<210> 1329

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1329

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgcg 180
tgcgagtggg tggcgagggc gggtgcaag ggtgaaccga ttacggcg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aagaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1330

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1330

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```


			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250						255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450														

530		535		540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 1331
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1331

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtggtta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccacaaa	gaggaagtgc	tgacgcgcgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tgttcgtgcg	360
ggtatgctgc	tgcgatgcga	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggtttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tggtgagcga	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgtctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgagatcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tggtgaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgttttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
tcgaaagagc	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	cagcgttggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1332
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1332

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1333

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1333

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgctcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg caggtgcgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1334
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1334
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 1335

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1335

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatc 1686

```

<210> 1336
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1336
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```

Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245				250						255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1337

<211> 1686

<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1337

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg aaaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
```

<210> 1338

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1338

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50					55					60				
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn	Asn 100	Leu	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Lys	Lys
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg	Ala 125	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr 175	Gly
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala 200	Leu	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln 285	Gly	Ser
Arg 290	Leu	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp 310	Arg	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu 335	Ile
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala 350	Gly	Asn
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe	Met 360	Gly	Gln	Tyr	Ile	Gly 365	Thr	Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu	Thr 390	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu 415	Lys
Gly	Leu	Gln	Ile	Thr 420	Gly	Asn	Ser	Ile	Met 425	Pro	Leu	Leu	Thr	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp

				485						490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
			500						505				510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp				
		515					520					525							
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535						540							
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545					550					555					560				
Ser	Ile																		

<210> 1339
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1339

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgtctgt	gaccgacaaa	gaggaagtgc	tcagcgcgt	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccaactg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacgggat	tgcggaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccag	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gtagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcgggtgg	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1340

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1340

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1341

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1341

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagcgctg	taacgcgagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tggtcgtgctg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccaactg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagaaccgat	ccaagatcgt	tacagcctgc	gttgcctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagatcga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatc
1686

```

<210> 1342
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1342
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Glu	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325				330						335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390					395						400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420				425							430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500				505						510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550				555						560			
Ser	Ile																

<210> 1343

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1343

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120

```

tatggtgcga aggcgctgct gaccaccaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcgggta cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagga aaaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1344
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1344
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```


His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
						535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1345
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1345
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1346
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1346
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		


```

agcaaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatacac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcatt 1686

```

```

<210> 1348
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 1348
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320

```

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1349

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1349

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660

```

```

ggtagcgagg tgatgaccgg tattgaggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctcgcgc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1350
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1350
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1351

```
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccactaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgcttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtgc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686
```

<210> 1352

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1352

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
```

Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			

Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1353
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1353

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggcca	ggttgcgct	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tcagcgct	taacagcagc	180
tgcgagtggg	tggcgaggc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtaggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgctcgctgcg	360
ggtatgctgc	tgctgagaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacgcttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctgggtggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgtctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgcttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	gatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1354
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1354

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro

385					390					395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1355

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1355

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200

```

```

gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgct 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1356
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1356
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270

```

Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455						460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550					555						560	
Ser	Ile															

<210> 1357

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1357

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgtgctg gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300

```

```

ctgatgcgtt atcacaaagc ggggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacagtgtt cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaagcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1358

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1358

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly

```


145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
				500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
				515					520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530					535					540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1359
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1359
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taactcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacgcttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgcctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1360
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1360
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30

Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr	
	35						40				45					
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115				120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					

Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1361

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1361

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgctg	120
tatgggtgca	aggcgcgtct	gaccacaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaagctgc	cgctggcgga	tgcttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacgggtgca	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgtctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcttgcc	gcagtatacc	960
ggcccattg	cggacgggat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcca	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcaccgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaagcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcgacggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1362
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1362
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn


```

atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgag 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagc 1686

```

<210> 1364
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1364
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220

```

Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ser																		

<210> 1365

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1365

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacggttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatc 1686
```

<210> 1366

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1366

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
```

			100					105				110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

530	535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala	Ile Asn Gln Val Val	
545	550	555
Ser Ile		

<210> 1367
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1367
 atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
 tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccaactg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtag cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacag cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaagcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcatt 1686

<210> 1368
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1368

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	

Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1369

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1369

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taactcgagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcaaac 1380

```

```

ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcaccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1370
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1370
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu

```

290		295		300
Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr				
305		310		320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val				
	325		330	335
Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn				
	340		345	350
Ala Ser Tyr His Gly Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser				
	355		360	365
Met Asp Arg Leu Arg Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp				
	370		375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro				
385		390		400
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys				
	405		410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr				
	420		425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn				
	435		440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg				
	450		455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Asp Lys Glu Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		555
Ser Ile				560

<210> 1371

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1371

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacagcgac 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480

```

```

agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

```

<210> 1372
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1372
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175

```


Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
		515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ile															

<210> 1373

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1373

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgcaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
tcgaaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatc
```

<210> 1374

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1374

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
```

	50				55				60							
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80	
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu	
Leu	Gln	Asn	Asn	Leu 100	Met	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly 120	Met	Leu	Leu	Arg	Ala	Asn	Ser	
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile	
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160	
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175	
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn	Gly	Glu	
Glu	Met	Thr 195	Ala	Pro	Glu	Ala	Leu 200	Lys	Leu	Leu	Gly 205	Leu	Glu	Pro	Leu	
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val	
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240	
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn	Gly 255	
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro	
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
Arg 290	Leu	Ile	Arg	Asp	Glu 295	Leu	Asp	Gly 300	Ser	His	Asp 305	Tyr	Arg	Gly	Glu 310	
Gln 305	Pro	Ile	Gln	Asp	Arg 310	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320	
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu 330	Ile	Ala	Lys 335	Gln	Ile	Glu	Ile 340	
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp 350	Val	Ala	Gly	Asn 355	
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr 365	Ile	Gly	Thr	Ser 370	
Met	Asp	Arg	Leu	Arg	Tyr 375	Tyr	Leu	Gly 380	Leu	Leu	Ala 385	Lys	His	Leu	Asp 390	
Val 385	Gln	Ile	Ala	Leu	Leu 390	Thr	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400	
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg 410	Pro	Val	Asn	Met	Gly	Leu	Lys 415	
Gly	Leu	Gln	Ile 420	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr 430	
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala 445	Glu	Gln	Phe	Asn 450	
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg 465	
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	

```
<210> 1375
<211> 1686
<212> DNA
<213> Artificial Sequence
```

<400> 1375						
atgatcattg	cgagccagac	caaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgctg	120
tatggtgcga	aggcgcgtct	gaccaccaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaa	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcaciaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcgtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	cacccggtc	aaatttgagg	cgcgcagcaa	840
atgctggagc	tgctgcaggg	cagccgtctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcttgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccaagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcaccctgca	actgtatctg	gcgattaagg	aagtgggttg	taaagcgccg	1560
gataaagatc	gtccgtatat	ctggaacgac	aatgagcagg	cgctggatga	acacattgctg	1620
ctgatcgagg	aggatatcac	cagcgacggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcatt						1686

<210> 1376

<211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1376

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			

Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ile														

<210> 1377

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1377

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgctgct	gaccacaaa	gaggaagtgc	tgcagcgctg	taacagcagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaga	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccgtctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagatcga	aatcaacagc	1020

```

gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagagc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1378

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1378

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly

```

				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310					315						320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Glu	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555					560			
Ser	Ile																

<210> 1379

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1379

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120


```

tatggtgcga aggcgcgtct gaccaccaa gaggaagtgc tgcagcgcgt taacagcagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggatga cctgaccccg ctggcgatga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaat tgaccgcgcc ggaggcgtg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccgtctg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
gataaagatc gtccgtatat ctggaacgac gatgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac cagcgacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt
1686

```

<210> 1380
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1380
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125

```

His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Arg	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
					295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
		370				375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
					455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asp	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
					535						540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560

Ser Ile

<210> 1381
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1381
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgcgt 120
tatgggtgcga aggcgctgct gaccacaaa gaggaagtgc tgcagcgctg taacagcagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccaactg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaagcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcatt 1686

<210> 1382
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1382
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His

1				5					10					15			
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr		
		35					40					45					
Thr	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
		130				135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
		210				215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
		290				295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
		370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		

gataaagatc gtccgtatat ctggaacgac aatgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatatacac cagcggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
 agcatt 1686

<210> 1384
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1384
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Thr Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Arg Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320

Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Asp	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ile														

<210> 1385

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1385

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aagcgtgctg gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgctggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aagcgtctgg gtctggagcc gctggagctg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720

```

```

gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgcaacaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaacgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gcagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1386
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1386
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195         200         205

```


Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Gln	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Glu	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1387

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1387

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgcgc gcgcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtgga tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgag tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca gctgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1388

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1388

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Arg Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu

```

				85					90					95				
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys			
				100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser			
				115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile			
				130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly			
				145					150					155				
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly			
				165					170					175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu			
				180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu			
				195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
				210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu			
				225					230					235				
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly			
				245					250					255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro			
				260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser			
				275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu			
				290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr			
				305					310					315				
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile			
				325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn			
				340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser			
				355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp			
				370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro			
				385					390					395				
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys			
				405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr			
				420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn			
				435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg			
				450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly			
				465					470									

	515		520		525										
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1389
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1389

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgctg	120
tatggtgcga	aagcgctgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggt	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcgtaca	tcaccgggtgc	gctggttggt	540
ctgaacgaca	gttataacctg	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacgggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atggggcagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaacgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaac	1380
ctgacccgtc	gcagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagtcaatgt	1500
ctgagcccgc	gcacccgtca	gctgtatctg	gcgattaagg	aagtggttgg	taaggcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcgggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1390
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1390

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35				40						45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400

Ala	Ser	Leu	Val	Gly	Asn	Thr	Glu	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1391

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1391

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggc 240
ttcggtagga tggcgcaagc gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgcttcgtgcg 360
ggatatgctg tcgctgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggc 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aagcgtctgg gtctggagcc gctggagctg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gctgtagacc tgggtgcaag tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaaacaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg aacaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260

```

```

accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagtcaatgt 1500
ctgagcccg cgcacccgtca gctgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1392
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1392
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser

```



```

ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aagctgctgg gtctggagcc gctggagctg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagtcaatgt 1500
ctgagcccg gcacccgtca gctgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1394
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1394
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Arg Ala Leu Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160

```

Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215				220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235				240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470						475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		

<210> 1395
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1395
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aatcgtctgg gtctggagcc gctggagctg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg aacaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gcagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagtcaatgt 1500
ctgagcccg gcacccgtcg tctgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1396
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1396
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr

		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Asn	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
		195				200						205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Asn	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390											

465		470		475		480									
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Arg	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555				560	
Ser	Ser														

<210> 1397

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1397

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgctcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aagcgtctgg gtctggagcc gctggagctg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1398
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1398
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350


```

taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtataa gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1400

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1400

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu

```


225					230					235				240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn
				245					250					255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His
			260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly
		275					280					285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly
	290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr
305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu
	370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu
385					390					395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu
				405					410					415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe
			420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe
	435						440					445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg
	450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe
465					470					475				480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr
				485					490					495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala
			500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile
		515					520					525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala
	530					535					540			
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val
545					550					555				560
Ser	Ser													

<210> 1401

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1401

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccca gggtgcgctg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagggcgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc ggggtgcgggc aagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgctggc aactgcgttc atgatgctga gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgctg aggatatac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1402
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1402
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110

```

Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser			
		115					120					125						
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile			
	130					135					140							
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly			
145				150						155					160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly			
				165					170						175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu			
			180				185						190					
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu			
		195					200					205						
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
		210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu			
225				230						235					240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly			
				245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro			
			260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser			
		275					280						285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu			
	290					295					300							
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr			
305				310						315					320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile			
				325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn			
			340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser			
		355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp			
	370					375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro			
385				390						395					400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys			
				405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr			
			420					425					430					
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn			
		435					440					445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg			
						455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly			
465					470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp			
				485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile			
			500					505					510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp			
		515					520					525						
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu			
	530					535					540							

Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1403
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1403
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tggtcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacgggtg caaccagagc 780
 ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtt tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
 agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
 ctgatcgcgg aggatattac cagtgcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1404
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1404

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr

Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370					375						380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500				505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ser															

<210> 1407

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1407

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccca gggtgcgctg 120
tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtgc tcaccggtgc gctgggttgg 540

```



```

ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1408

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1408

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
          145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu

```


<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1409

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc ggggtgcggg aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacggttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttcacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1410

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1410

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
        35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
       50          55          60
```

Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	65	70	75	80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	85	90	95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	100	105	110	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	115	120	125	
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	130	135	140	
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170	175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	

Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1411
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1411

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	tggtgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcaaggcgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	cacccggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccatttg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgagatcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccag	atattggtag	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgccctgctg	acctatgccg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagtggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1412
 <211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1412

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp

370	375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro		
385	390	395
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys		
405	410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr		
420	425	430
Gly Asn Ser Leu Thr Asp Arg Phe Gly Ser Ala Asn Leu Thr Arg Arg		
435	440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg		
450	455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly		
465	470	475
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp		
485	490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile		
500	505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp		
515	520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu		
530	535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val		
545	550	555
Ser Ser		

<210> 1413
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1413
 atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggcca ggttgcgcgt 120
 tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
 ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccattg cggaaggatg tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080

```

atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1414
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1414
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255

```


Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325					330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355						360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485						490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1415

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1415

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180

```

```

tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcggg tggttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagggaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 1416
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1416
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile

```

[illegible]

<210> 1417
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1417
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggtta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgctttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccgggtg gctggttggg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttgtag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
 ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
 agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
 ctgatcgagg aggatcac cagtggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1418
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1418
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15

Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr		
		35					40					45					
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
	50					55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390						395				400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					

Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1419

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1419

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccca ggttgcgctg 120
tatggtgcca aggcgcgtct gaccgacaaa gaggaagtgc tgcagggcgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggc 240
ttcggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca ca tgtgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagatt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttgg 1440
gtgaaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcaaatgt 1500
ctgagccgca gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620

```

ctgatcgcgaggatattcac cagtgacggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
 agcagt 1686

<210> 1420
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1420
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Val Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile


```

gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgaggatattcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 1422
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1422
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205

```

Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1423

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1423

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagggcgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtgga tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacctgct gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caaagacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1424

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1424

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu

```

										85					90					95				
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys									
			100					105					110											
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser									
		115					120					125												
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile									
		130				135					140													
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly									
145				150					155					160										
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly									
			165						170					175										
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu									
			180					185					190											
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu									
		195				200					205													
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val									
		210				215					220													
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu									
225				230					235					240										
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly									
			245					250						255										
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro									
			260				265						270											
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser									
		275				280						285												
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu									
		290				295					300													
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr									
305				310					315						320									
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile									
			325					330					335											
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn									
			340				345						350											
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser									
		355				360						365												
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp									
		370				375					380													
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro									
385				390					395			</												

	515		520		525										
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1425
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1425

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagggcgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caacaaaaac	atcaacagcc	agggtttttg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1426
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1426

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400

Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1427

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1427

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260

```

```

accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaaacc atcaacagcc agggtttttg cagcgcgaaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1428
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1428
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser

```



```

ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagtggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1430
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1430
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160

```

Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215				220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235				240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		

<210> 1431
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1431
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1432
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1432
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr

		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195				200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390				</							

465		470		475		480									
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1433
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1433

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtggtta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	tggttgcgct	120
tatggtgcga	aggcgtgct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggtgcgaag	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggtgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccgtg	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgagatcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggtcaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tggttaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcaccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1434
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1434
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350

Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1435

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1435

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgcgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggttggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tcgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900


```

taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtatac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgac 1620
ctgatcgcgg aggatatac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1436

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1436

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu

```

225					230					235				240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn Gly
				245					250					255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His Pro
			260					265						270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln Gly	Ser
		275					280					285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg Gly	Glu
	290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln Tyr	Thr
305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile Glu	Ile
				325				330						335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala Gly	Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly Thr	Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385					390					395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu Lys
			405						410					415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr Phe	Tyr
		420						425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln Phe	Asn
	435						440					445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr Arg	Arg
	450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met Phe	Gly
465					470				475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His Tyr	Asp
			485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu Ala	Ile
			500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr Ile	Trp
		515					520					525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile Ala	Glu
	530					535					540			
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln Val	Val
545					550					555				560
Ser	Ser													

<210> 1437

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1437

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccca gggtgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgctggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgctggc aactgctgtc atgatgctga gaacctgctg 720
gctgtagctg tgggtgctga tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccc caccgggtgc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgctg gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgctg aggatatac cagtgcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1438

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1438

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110

```

Leu 115	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
His 130	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
Met 370	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln 450	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu

Asp Ile Thr Ser Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ser

<210> 1439
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1439
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccca gggtgcgctg 120
 tatggtgcca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaagc gggtgctggc cagaagctgc cgctggcggg tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
 agcatcgggt cgagcgggtg cctgaccccg ctggcgctaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
 ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtg tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgacctgct gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
 ctgatcgcgg aggatattac caaagacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1440
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1440

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr


```

gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgaggatatacac caaagacggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 1442
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1442

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85						90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100						105				110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180				185						190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195					200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				

Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305		310		315		320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		325		330		335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		340		345		350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		355		360		365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		370		375		380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385		390		395		400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		405		410		415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		420		425		430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		435		440		445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		450		455		460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465		470		475		480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		485		490		495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		500		505		510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		515		520		525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu		530		535		540	
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545		550		555		560
Ser	Ser																					

<210> 1443

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1443

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccca gggtgcgctg 120
tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540

```

```

ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1444
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1444
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu

```


<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1445

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcaciaaagc ggggtgcggg aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccagcag 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctg gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1446

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1446

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
        35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
       50          55          60
```

Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	65	70	75	80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	85	90	95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	100	105	110	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	115	120	125	
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	130	135	140	
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170	175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	

Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1447
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1447

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggcca	ggttgcgct	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tgctctgtcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccgggtg	gctgggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttgtag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	acctatgccg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagagc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1448
 <211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1448

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp

370	375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro		
385	390	395
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys		
405	410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr		
420	425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn		
435	440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg		
450	455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly		
465	470	475
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp		
485	490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile		
500	505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp		
515	520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu		
530	535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val		
545	550	555
Ser Ser		

<210> 1449

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1449

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggcca	ggttgcgct	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tggtcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgagatcga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080


```

atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caagacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1450
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1450
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255

```



```

tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcggg tggttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgagggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgtatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1452
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1452
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1          5          10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile

```

[illegible]

<210> 1453
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1453
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggtta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggc 240
 ttcggtggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgacgctttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccattg cgacgggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
 ccgaccacg cgagcaggtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgagg aggatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1454
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1454
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15

Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile	
			20					25					30			
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr	
		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				

Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1455

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1455

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc tgttgcgctg 120
tatggtgcca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcgggc aactgcgttc atgatgcaaa gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccc caccgggttc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtcca gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaa gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cgagcagatt caacaaaac atcaacagcc aggggttttg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaacg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcaaatgt 1500
ctgagccgca gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620

```

ctgatcgcgaggatattcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
 agcagt 1686

<210> 1456
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1456
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val


```

gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1458
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1458
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205

```

Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1459

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1459

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc tgttgcgctg 120
tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgacccc ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1460

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1460

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu

```

				85					90					95				
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys			
				100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser			
				115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile			
				130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly			
				145					150					155				
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly			
				165					170					175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu			
				180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu			
				195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
				210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu			
				225					230					235				
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly			
				245					250					255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro			
				260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser			
				275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu			
				290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr			
				305					310					315				
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile			
				325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn			
				340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser			
				355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp			
				370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro			
				385					390					395				
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys			
				405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr			
				420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn			
				435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg			
				450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly			
				465					470									

	515		520		525										
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1461
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1461

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccgc	tgttgcgcg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tcagcgcgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaca	tcaccggtgc	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcctgcc	gcagtatacc	960
ggcccgattg	cggacgggtat	tgcggaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaaccttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagagc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattcgc	1620
ctgatcgcg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1462
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1462

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400

Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1463

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1463

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagggcgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggc 240
ttcggtaggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgctgagcaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggc 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gctgtagcgc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260

```



```

accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1464
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1464
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser

```



```

ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctgggttggg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagtggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1466

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1466

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160

```

Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215				220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		

<210> 1467
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1467
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgatttttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgccg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1468
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1468
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr

		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390					</							

465		470		475		480									
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555				560	
Ser	Ser														

<210> 1469
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1469

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtggtta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tggttgcgct	120
tatggtgcga	aggcgtgct	gaccgacaaa	gaggaagtgc	tgcagggcgt	taacgcgagc	180
tgcgagtggg	tggtgcgaag	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggtgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tggtgctgca	tgctgctggc	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggtcaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgctgctgct	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tggttaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcaccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattcgc	1620
ctgatcgcgg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1470
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1470
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350

Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1471

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1471

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgcgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggttggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900

```

taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tcaggaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtatac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgac 1620
ctgatcgcgg aggatatac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1472

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1472

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu

```

225					230					235				240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn
				245					250					255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His
			260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly
		275					280					285		Ser
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly
	290					295					300			Glu
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr
305				310						315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Gln	Glu	Ile	Ala	Lys	Gln	Ile	Glu
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly
			340					345					350	Asn
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr
		355					360					365		Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu
	370					375					380			Asp
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu
385					390					395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu
			405						410					415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe
			420					425					430	Tyr
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe
	435						440					445		Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg
	450					455					460			Arg
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe
465					470					475				480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr
			485						490					495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala
			500					505					510	Ile
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile
		515					520					525		Trp
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala
	530					535					540			Glu
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val
545					550					555				560
Ser	Ser													

<210> 1473

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1473

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccc caccgggttc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatac cagtggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1474
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1474
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110

```

Leu 115	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
His 130	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
Ser 160	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
Ala 180	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu 195	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
Ala 245	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
Thr 260	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
Gly 275	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Gln 290	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
Gly 325	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
Glu 340	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala 355	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
Met 370	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
Ala 405	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
Gly 420	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
Gly 435	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln 450	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
Val 485	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
Ala 500	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
Lys 515	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
Asn 530	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu

Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1475
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1475
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccca gggttgcgct 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagggcgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggttgcgaag ggtgaaccga ttacggcgt taccactgg 240
 ttcgggtggca tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggttgcgggc aagaagctgc cgctggcggg tggttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggcg aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
 agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1476
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1476

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
					215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr


```

gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgaggatatacac caaagacggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 1478
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1478

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35				40						45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50				55				60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100					105						110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180				185						190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195					200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				

Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305			310		315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile				325		330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn				340		345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser				355		360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp				370		375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro				385		390					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys				405		410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr				420		425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn				435		440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg				450		455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly				465		470					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp				485		490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				500		505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp				515		520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu				530		535					540	
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				545		550					555	
Ser	Ser																										

<210> 1479

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1479

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc tgttgcgctg 120
tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540

```

```

ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caagacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1480

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1480

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
          145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu

```


<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1481

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggcca gggtgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccagcag 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1482

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1482

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
        35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
       50          55          60
```

Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385						390				395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	

Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1483

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1483

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgct 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagggcgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattcgggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg acctgcccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac cagtggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1484

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1484

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp

370	375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro		
385	390	395
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys		
405	410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr		
420	425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn		
435	440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg		
450	455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly		
465	470	475
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp		
485	490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile		
500	505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp		
515	520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Arg Leu Ile Ala Glu		
530	535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val		
545	550	555
Ser Ser		

<210> 1485
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1485

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgccgct	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgctg	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tggtcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggttc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080

```

atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caagacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1486
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1486
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255

```



```

tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagggaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tcaggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgagg aggatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1488

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1488

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile

```

[illegible]

<210> 1489
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1489
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggtta ttgtgggtga taagccgctg acgatcaagg aggtggcca ggttgcgctg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cgagcaggtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaacg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatattac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1490
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1490
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15

Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile	
			20					25					30			
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr	
		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				

Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1491

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1491

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggc 240
ttcggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgctg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggtggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgca gaacctgctg 720
gcgctgagcc tgggtgca caacgctggc ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcaaatgt 1500
ctgagccgca gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620

```


ctgatcgcgaggatattcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
 agcagt 1686

<210> 1492
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1492
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Lys Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val


```

gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1494
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1494
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205

```

Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1495

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1495

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccca ggttgcgcgt 120
tatggtgcca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtgcca tggcgcaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgag ggctgaccc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgacggg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccc caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgagg aggatattac cagtgcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1496

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1496

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu

```

				85				90				95			
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
100				105				110							
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
115				120				125							
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130				135				140							
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
165				170				175							
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
180				185				190							
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
195				200				205							
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210				215				220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
245				250				255							
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
260				265				270							
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
275				280				285							
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290				295				300							
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
325				330				335							
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
340				345				350							
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
355				360				365							
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370				375				380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
405				410				415							
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
420				425				430							
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
435				440				445							
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450				455				460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470				475				480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
485				490				495							
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
500				505				510							
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp

	515		520		525										
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1497
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1497

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcg	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgctggc	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgagatcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaaccttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgacccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattcgc	1620
ctgatcgcg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1498
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1498

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400

Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1499

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1499

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tcgctgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260

```

```

accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1500
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1500
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Lys Glu Val Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser

```



```

ggtatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tcaggaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1502
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1502
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160

```

Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215				220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235				240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Gln	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		

<210> 1503
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1503
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tcaggaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcg aggatcac cagtacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1504
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1504
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr

		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195				200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Gln	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390											

465		470		475		480									
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555				560	
Ser	Ser														

<210> 1505

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1505

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgccaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgctcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```


<210> 1506
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1506
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350

Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1507

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1507

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccca	ggttgcgctg	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcggaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggttggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccgt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900

```

taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caaagacggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1508

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1508

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu

```

225					230					235				240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn Gly
				245					250					255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His Pro
			260					265						270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln Gly	Ser
		275					280					285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg Gly	Glu
	290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln Tyr	Thr
305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile Glu	Val
				325				330						335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala Gly	Asn
			340				345						350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly Thr	Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His Leu	Asp
	370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly Leu	Pro
385					390					395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly Leu	Lys
				405					410					415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr Phe	Tyr
			420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln Phe	Asn
		435					440					445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr Arg	Arg
	450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met Phe	Gly
465					470					475				480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His Tyr	Asp
				485					490					495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu Ala	Ile
			500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr Ile	Trp
		515					520					525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile Ala	Glu
	530					535					540			
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln Val	Val
545					550					555				560
Ser	Ser													

<210> 1509

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1509

```

atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgctggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgctggc aactgctgtc atgatgctga gaacctgctg 720
gctgtagctg tgggtgctga tgcgctggcg ctgcaggggc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccgggtgc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcaagcaaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgctgc gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcaaac actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagagc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgct 1620
ctgatcgctg aggatattac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1510
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1510
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110

```

Leu 115	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
His 130	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
Ser 160	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
Ala 180	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu 200	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
Ala 245	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
Thr 260	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
Gly 275	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Gln 290	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
Gly 325	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
Glu 340	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala 355	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
Met 370	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
Ala 405	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
Gly 420	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
Gly 435	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln 450	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
Val 485	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
Ala 500	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
Lys 515	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
Asn 530	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu

Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ser

<210> 1511
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1511
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgctg taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgctgt atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgacctg cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtg cctgaccccg ctggcgatga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtg tgctgaaatc gcgaagcaaa tcgagatcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatattac cagcgtgggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1512
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1512

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr


```

gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgaggatatacac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 1514
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1514

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85						90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180				185						190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				

Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370				375						380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500				505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ser															

<210> 1515

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1515

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcaggcgct taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaag ggtgaaccga ttacggcgct taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccggtgc gctgggttgg 540

```

```

ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1516
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1516
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu

```


<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1517

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca gggtgcgct 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcacccgtt ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccagcag 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaacg ctatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1518

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1518

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
        35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
       50          55          60
```

Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
		290				295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385						390				395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ala	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	

Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1519
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1519

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	agggtggcca	ggttgcgcgt	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggatgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgcctcggt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgctcgtgcg	360
ggatatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccgtg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccag	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	acctatgccg	agtttaacaa	cggtctgccg	1200
gtagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaagg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcggttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1520
 <211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1520

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp

370	375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro		
385	390	395
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys		
405	410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr		
420	425	430
Gly Asn Ser Leu Thr Asp Arg Phe Gly Ser Ala Asn Leu Thr Arg Arg		
435	440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg		
450	455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly		
465	470	475
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp		
485	490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile		
500	505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Glu Arg Pro Tyr Ile Trp		
515	520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu		
530	535	540
Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val		
545	550	555
Ser Ser		

<210> 1521
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1521

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggcca	ggttgcgct	120
tatggtgcga	aggcgtgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tggtcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccgt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080

```

atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggc gctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1522
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1522
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255

```

Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325					330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Ala	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1523

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1523

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgct 120
 tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180

```

tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcggg tggttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cagcgtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagggaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tgtgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 1524
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1524
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile

```

[illegible]

<210> 1525
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1525
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggcca ggttgcgctg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgacgcttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgctaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagctg 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcaaatgt 1500
ctgagccgcg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatattac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1526
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1526
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15

Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile	
			20					25					30			
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr	
		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Leu	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				

Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1527

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1527

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccc caccgggttc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctgcgctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cgagcagatt caacaaaac atcaacagcc aggggttttg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaacg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcaaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620

```

ctgatcgcgaggatatacac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
 agcagt 1686

<210> 1528
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1528
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile


```

gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg aatatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgaggatattcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 1530
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1530
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205

```

Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1531

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1531

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgcttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgacccc ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accgctccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cccccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1532

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1532

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu

```

				85					90					95				
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys			
				100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser			
				115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile			
				130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly			
				145					150					155				
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly			
				165					170					175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu			
				180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu			
				195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
				210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu			
				225					230					235				
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly			
				245					250					255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro			
				260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser			
				275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu			
				290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr			
				305					310					315				
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile			
				325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn			
				340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser			
				355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp			
				370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Ala	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro			
				385					390					395				
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys			
				405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr			
				420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn			
				435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg			
				450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly			
				465					470									

	515		520		525										
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535					540					
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1533
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1533

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgctg	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgcctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1534
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1534

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Lys	Glu	Val	Ala	Gln	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35				40						45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100					105						110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400

Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1535

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1535

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca ggttgcgctg 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtaggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgcttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaaacg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260

```

```

accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1536
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1536
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Thr Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser

```



```

ggtatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgtt aacgagcagg cgctggatga acacattgag 1620
ctgatcgcgg aggatatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1538

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1538

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160

```

Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly			
				165					170					175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu			
			180					185					190					
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu			
		195					200					205						
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
	210				215						220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu			
225				230						235				240				
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly			
			245					250					255					
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro			
		260					265						270					
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser			
	275					280						285						
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu			
	290				295						300							
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr			
305				310						315					320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile			
			325					330					335					
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn			
		340					345					350						
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser			
	355					360					365							
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp			
	370				375					380								
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro			
385				390						395				400				
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys			
			405					410					415					
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr			
		420					425					430						
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn			
	435					440						445						
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg			
	450				455					460								
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly			
465				470					475					480				
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp			
			485					490					495					
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile			
		500					505					510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp			
	515					520						525						
Asn	Val	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu			
	530				535						540							
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val			
545				550					555					560				
Ser	Ser																	

<210> 1539
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1539
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgcgt 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tggtcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcattc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatcac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1540
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1540
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr

	35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170				175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185				190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195				200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250				255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Ile	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
			325						330				335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345				350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						3					

465		470		475		480									
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1541
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1541

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtggtta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgctg	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccgg	cttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcctgcc	gcagtatacc	960
ggcccgattg	cggacgggtat	tgcggaaatc	gcgaagcaaa	tcgagattga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcaccgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagaac	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	cagcggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1542
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1542
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ala Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Ile
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350

Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1543

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1543

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaagg	aggtggccca	ggttgcgcgt	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcggaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggttggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttc	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900

```

taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gctttaaggg tctgcagatt 1260
accggtatac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgag 1620
ctgatcgcgg aggatatac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1544

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1544

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val His Asp Ala Gln Asn Leu Leu

```

225					230					235				240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn
				245					250					255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His
			260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly
		275					280					285		Ser
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly
	290					295					300			Glu
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr
305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu
				325				330						335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly
			340					345					350	Asn
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr
		355					360					365		Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu
	370					375					380			Asp
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu
385					390					395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Phe
			405						410					415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe
			420					425					430	Tyr
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe
	435						440					445		Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg
	450					455					460			Arg
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe
465					470				475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr
			485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala
			500					505					510	Ile
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Glu	Arg	Pro	Tyr	Ile
		515					520					525		Trp
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala
	530					535					540			Glu
Asp	Ile	Thr	Ser	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val
545					550					555				560
Ser	Ser													

<210> 1545

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1545

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaagg aggtggccca gggtgcgctg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcggg tggtcgtgctg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgctggc aactgcgttc atgatgcgca gaacctgctg 720
gctgtagctg tgggtgctga tgcgctggcg ctgcaggggc tgaacgggtg caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aacaaccgat ccaagatcgt tacagcctgc ggtgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgctg aggatattac cagcggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1546
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1546
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Lys Glu Val Ala Gln Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110

```

Leu 115	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu 125	Arg	Ala	Asn	Ser
His 130	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu	Leu 140	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu	Met	Thr	Ala 195	Pro	Glu	Ala	Leu	Lys 200	Leu	Leu	Gly	Leu 205	Glu	Pro	Leu
Glu	Leu 210	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	His	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn	Gly 255
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln 280	Met	Leu	Glu	Leu	Leu 285	Gln	Gly	Ser
Gln	Leu 290	Ile	Arg	Asp	Glu	Leu	Asp 295	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp	Arg 310	Tyr	Ser	Leu	Arg	Cys 315	Leu	Pro	Gln	Tyr	Thr 320
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile 330	Ala	Lys	Gln	Ile	Glu	Ile 335
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro 345	Leu	Ile	Asp	Val	Ala	Gly	Asn 350
Ala	Ser	Tyr 355	His	Gly	Gly	Asn	Phe 360	Met	Gly	Gln	Tyr	Ile 365	Gly	Thr	Ser
Met	Asp 370	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala 380	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu	Thr 390	Met	Pro	Glu	Phe 395	Asn	Asn	Gly	Leu	Pro 400
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro 410	Val	Asn	Met	Gly	Leu	Lys 415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile 425	Met	Pro	Leu	Leu	Thr	Phe	Tyr
Gly	Asn	Ser 435	Leu	Thr	Asp	Arg	Phe 440	Pro	Thr	His	Ala	Glu 445	Gln	Phe	Asn
Gln	Asn 450	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn 460	Leu	Thr	Arg	Arg
Ser 465	Ile	Glu	Ile	Phe	Gln 470	Gln	Tyr	Ile	Ala	Ile 475	Ala	Leu	Met	Phe	Gly 480
Val	Gln	Ser	Val	Asp 485	Leu	Arg	Thr	Lys	Lys 490	Ile	Ala	Asn	His	Tyr	Asp 495
Ala	Ser	Gln	Cys 500	Leu	Ser	Pro	Arg	Thr 505	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
Lys	Glu	Val 515	Val	Gly	Lys	Ala	Pro 520	Ser	Lys	Glu	Arg	Pro 525	Tyr	Ile	Trp
Asn	Asp 530	Asn	Glu	Gln	Ala	Leu	Asp 535	Glu	His	Ile	Ala 540	Leu	Ile	Ala	Glu

Asp Ile Thr Ser Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ser

<210> 1547
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1547
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatggtgctg gtgcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgctggc cagaagctgc cgctggcggg tgttcgtgctg 360
 ggtatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgctga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccc caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg cctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
 ctgatcgctg aggatattac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1548
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1548

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Arg	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr


```

ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg aacatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1552
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1552
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
          145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu

```


<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1553

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgct 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactgg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc ggggtgcggg aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttgg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttcacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggc cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1554

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1554

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
        35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
       50          55          60
```

Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385						390				395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Ala	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	

Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1555
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1555

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgctg	gtgcgctgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgctggc	aagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccatttg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccag	atattggtag	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	aacatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	cctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattcgt	1620
ctgatcgctg	aggatatcac	caaaggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1556
 <211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1556

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Arg	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp

370	375	380
Val Gln Ile Ala Leu Leu Asn Met Pro Glu Phe Asn Asn Gly Leu Pro		
385	390	395
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys		
405	410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr		
420	425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn		
435	440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg		
450	455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly		
465	470	475
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp		
485	490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile		
500	505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp		
515	520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Arg Leu Ile Ala Glu		
530	535	540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val		
545	550	555
Ser Ser		

<210> 1557
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1557

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcg	120
tatggtgcga	aggcgtgctg	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgctgt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tggtcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggt	540
ctgaacgaca	gttataacctg	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccgtg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080

```

atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg aacatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620
ctgatcgcgg aggatatcac caagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1558
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1558
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255

```

Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470					475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ser														

<210> 1559

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1559

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgct 120
tatggtgcgc gtgcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180

```

```

tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc ggggtcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgagggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg aacatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1560
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1560
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
           20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Leu Leu Thr
           35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
           50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
           85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
           100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
           115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile

```

[illegible]

<210> 1561
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1561
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggtta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg aacatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaacgc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcaaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1562
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1562
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15

Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile	
			20					25					30			
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr	
		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85				90						95		
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				

Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1563

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1563

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcg gtgcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg aacatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcaggtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgaaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcaaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620

```

ctgatcgcgaggatattcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
 agcagt 1686

<210> 1564
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1564
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Lys Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val


```

gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg aacatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgaggatattcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 1566
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1566
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205

```

Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1567

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1567

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcgc gtgcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgct atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gctgtgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacctgct aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caaagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1568

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1568

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu

```

				85					90					95			
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys		
				100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
				115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
				130					135					140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
				180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
				195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
				210					215					220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
				260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
				275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
				290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
				340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
				355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
				370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
				420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
				435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
				450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp													

	515		520		525										
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1569
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1569

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcg	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgcttcgtgc	360
ggatgctgc	tgctgcgaa	cagccacctg	caggtgcga	gcggtatccg	tctggagctg	420
attcagcgtg	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgctggc	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgcctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgctgctgct	aacatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgtca	actgtatctg	gcgattaagg	aagtggttgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgca	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1570
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1570

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400

Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1571

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1571

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtaggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcgga tgcttcgtgcg 360
ggatatgctg tgctgagcaa cagccacctg cacggtagca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gctgtagacc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260

```

```

accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1572
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1572
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser

```



```

ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620
ctgatcgcgg aggatatcac caagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1574
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1574
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160

```

Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215				220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235				240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		

<210> 1575
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1575
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcgggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgatttttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1576
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1576
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr

		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
			165						170				175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195				200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
			245						250				255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
		260						265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
			325						330				335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390					</							

465		470		475		480									
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555				560	
Ser	Ser														

<210> 1577

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1577

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgctcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg cctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcg aggatcac caaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1578
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1578
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350

Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1579

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1579

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcgt	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggttggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tcgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900

```

taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtatac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgctca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1580

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1580

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu

```

225					230					235				240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn
				245					250					255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His
			260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly
		275					280					285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly
	290					295					300			
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr
305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu
	370					375					380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu
385					390					395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu
				405					410					415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe
			420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe
	435						440					445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg
	450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe
465					470					475				480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr
				485					490					495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala
			500					505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile
		515					520					525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala
	530					535					540			
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val
545					550					555				560
Ser	Ser													

<210> 1581

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1581

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgccaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc aagaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccc caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg aacatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1582
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1582
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
           20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
           35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
           50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
           85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
           100          105          110

```

Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				

Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ser

<210> 1583
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1583
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcgggtggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgctgt atcacaaagc gggtgcgggc aagaagctgc cgctggcggg tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgatga tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacgggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg cctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
 ctgatcgcgg aggatattac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1584
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1584

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr


```

gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgaggatatacac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 1586
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1586

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85						90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
		260						265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				

Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305			310		315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val				325		330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn				340		345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser				355		360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp				370		375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro				385		390					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys				405		410					415	
Ala	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr				420		425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn				435		440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg				450		455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly				465		470					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp				485		490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				500		505					510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp				515		520					525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				530		535					540	
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				545		550					555	
Ser	Ser																										

<210> 1587

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1587

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540

```

```

ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1588

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1588

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
          145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu

```


<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1589

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcacccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcgacaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcaccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1590

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1590

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
        35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
       50          55          60
```


Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130						135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
		210				215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385						390				395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	

Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1591

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1591

```

atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgct 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggc 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg acctatgccg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1592

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1592

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp

370	375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro		
385	390	395
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys		
405	410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr		
420	425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn		
435	440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg		
450	455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly		
465	470	475
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp		
485	490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile		
500	505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp		
515	520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu		
530	535	540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val		
545	550	555
Ser Ser		

<210> 1593
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1593

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcgggtggc	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tggtcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080

```

atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg aacatgccgg agtttaacaa cggtctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cgagcagatt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1594
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1594
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255

```

Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470					475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ser														

<210> 1595

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1595

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180

```

```

tgcgagtggg tggcgcaagc ggttgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggca tggcgaaactt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cagcgtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg aacatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgtatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 1596
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1596
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile

```

[illegible]

<210> 1597
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1597
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgacgctttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgctaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaag tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgagggtcg aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaacg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcaaatg 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1598
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1598
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15

Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile	
			20					25					30			
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr	
		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				

Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1599

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1599

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcca aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggc 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccgggtg gctgggtggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaac tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggttc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccaat atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggc cctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cgagcagatt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagcaaatgt 1500
ctgagccgcg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620

```

ctgatcgcgaggatattcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
 agcagt 1686

<210> 1600
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1600
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val


```

gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg aacatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1602
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1602
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195         200         205

```

Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
		450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1603

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1603

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgctgt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tcggtgcgaa cagccacctg caggtgcgga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgag tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cccccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1604

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1604

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu

```


							85								90								95
Leu	Gln	Asn	Asn	Leu	Met	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys								
			100				105						110										
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser								
		115				120						125											
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile								
			130				135						140										
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly								
145				150						155			160										
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly								
			165						170			175											
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu								
			180			185						190											
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu								
		195				200						205											
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val								
		210				215						220											
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu								
225				230						235			240										
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly								
			245						250			255											
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro								
			260			265						270											
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser								
		275				280						285											
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu								
		290				295						300											
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr								
305				310						315			320										
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val								
			325			330						335											
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn								
			340			345						350											
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser								
		355				360						365											
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp								
		370				375						380											
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro								
385				390						395			400										
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys								
			405			410						415											
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr								
		420				425						430											
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn								
		435				440						445											
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg								
		450				455						460											
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly								
465				470						475			480										
Val	Gln																						

	515		520		525										
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1605
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1605

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccc	ctggcgtaca	tcaccgggtgc	gctggttggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgtggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttgc	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgctgtgctg	aacatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	cctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacctgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1606
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1606

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400

Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1607

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1607

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtaggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgcttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260

```

```

accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1608
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1608
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260    265    270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser

```



```

ggtatgctgc tgcgtgcaaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggtctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggc cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caaagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1610

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1610

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Arg Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Met Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160

```

Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215				220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Ala	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470						475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		

<210> 1611
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1611
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg aacatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1612
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1612
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr

		35					40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
	50					55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195				200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390				</							

465		470		475		480									
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1613
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1613

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tggtgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tcgagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgtt	atcacaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgcctgcc	gcagtatacc	960
ggcccgattg	cggacgggtat	tgctgaaatc	gcgaagcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	cctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacctgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1614
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1614
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Leu Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
 325 330 335
 Glu Ile Asn Ser Val Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn
 340 345 350

Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1615

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1615

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ttgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcgt	120
tatggtgcga	aggcgctgct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggttggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgatgcgct	atcacaaagc	gggtgcgggc	aagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tcgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccgtg	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900

```

taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg aacatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1616

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1616

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu

```

225					230					235				240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn
				245					250					255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His
			260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly
		275					280					285		Ser
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly
	290					295					300			Glu
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr
305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu
				325				330						335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly
			340					345					350	Asn
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr
		355					360					365		Ser
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu
	370					375					380			Asp
Val	Gln	Ile	Ala	Leu	Leu	Asn	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu
385					390					395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu
			405						410					Lys
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe
			420					425					430	Tyr
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe
	435						440					445		Asn
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg
	450					455					460			Arg
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe
465					470				475					Gly
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr
			485					490						Asp
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala
			500					505					510	Ile
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile
		515					520					525		Trp
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala
	530					535					540			Glu
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val
545					550					555				Val
Ser	Ser													

<210> 1617

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1617

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcg gtgcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc aagaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggttc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1618
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1618
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
           20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Leu Leu Thr
           35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
           50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
           85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
           100          105          110

```


Leu 115	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
His 130	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
Ser 160	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
Ala 180	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu 195	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
Ala 245	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
Thr 260	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
Gly 275	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Gln 290	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
Gln 305	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
Gly 325	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
Glu 340	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala 355	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
Met 370	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
Val 385	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
Ala 405	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
Gly 420	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
Gly 435	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln 450	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
Val 485	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
Ala 500	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
Lys 515	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
Asn 530	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu

Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val
 545 550 555 560
 Ser Ser

<210> 1619
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1619
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc gggtgcgggc aagaagctgc cgctggcggg tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
 ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1620
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1620

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Leu	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
						215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr


```

gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgaggatatacac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 1622
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1622
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Leu Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145      150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225      230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290      295     300

```

Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370					375						380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500				505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ser															

<210> 1623

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1623

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540

```

```

ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1624
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1624
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu

```


<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1625

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcggg aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcacccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca accgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggc cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcaccgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1626

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1626

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
        35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
       50          55          60
```

Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	65	70	75	80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	85	90	95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	100	105	110	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	115	120	125	
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	130	135	140	
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170	175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330	335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410	415	
Ala	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490	495	

Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1627

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1627

```

atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgct 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg acctatgccg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1628

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1628

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Met	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp

370	375	380
Val Gln Ile Ala Leu Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro		
385	390	395
Ala Ser Leu Val Gly Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys		
405	410	415
Gly Leu Gln Ile Thr Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr		
420	425	430
Gly Asn Ser Leu Thr Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn		
435	440	445
Gln Asn Ile Asn Ser Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg		
450	455	460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly		
465	470	475
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp		
485	490	495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile		
500	505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp		
515	520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu		
530	535	540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val		
545	550	555
Ser Ser		

<210> 1629
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1629
 atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgatgcgtt atcacaaagc ggggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcggtga cctgaccccg ctggcgta taccgggtgc gctggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
 ggcccattg cgagcggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080

```

atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1630
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1630
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255

```

Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355					360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390					395						400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420				425						430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435				440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470					475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500				505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550					555						560
Ser	Ser														

<210> 1631

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1631

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtggtta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgct 120
 tatggtgcga aggcgctgct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180

```

tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgatgcgtt atcacaaagc ggggtgcgggc aagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctgggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaacg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgt 1620
ctgatcgcgg aggatatcac caagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1632
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1632
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Ile Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Leu Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Met Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile

```


[illegible]

<210> 1633
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1633
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggtta ttgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcgc gtgcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggca tggcgaaact gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcaaaacctt cctgaacgcg ggcgtgacct cgacgctttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgctaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaata tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggc cctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaacgc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagcaaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaatgc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgagg aggatattac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1634
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1634
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15

Thr	Ala	Ser	Asp	Ser	Val	Val	Ile	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile		
			20					25					30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Arg	Ala	Arg	Leu	Thr		
		35					40					45					
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
		50				55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Ala	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					

Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1635

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1635

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcggc	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgctg	gcgcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacagtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccc	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgct	1620
ctgatcgcg	aggatatcac	caaaggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 1636

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1636

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Gly Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
      325     330     335

```

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1637

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1637

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aagcgctctt gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccactgt atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgctcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```

```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggccccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcgc 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1638

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1638

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala Leu Gln Gly	Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His Gln Cys Lys	Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu Glu Leu Leu Gln Gly	Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser His Asp Tyr Arg Gly	Glu
290	295	300
Gln Pro Ile Gln Asp	Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr	
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val	
325	330	335
Glu Ile Asn Ser Val Thr	Asp Asn Pro Leu Ile Asp Val Ala Gly Asn	
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser	
355	360	365
Met Asp Arg Leu Arg Tyr	Tyr Leu Gly Leu Leu Ala Lys His Leu Asp	
370	375	380
Val Gln Ile Ala Leu Leu Thr	Met Pro Glu Phe Asn Asn Gly Leu Pro	
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys	
405	410	415
Gly Leu Gln Ile Thr Gly	Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr	
420	425	430
Gly Asn Ser Leu Thr Asp	Arg Phe Pro Thr His Ala Glu Gln Phe Asn	
435	440	445
Gln Asn Ile Asn Ser Gln	Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg	
450	455	460
Ser Ile Glu Ile Phe Gln	Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly	
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp	
485	490	495
Ala Ser Gln Cys Leu Ser	Pro Arg Thr Cys Gln Leu Tyr Leu Ala Ile	
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp	
515	520	525
Asn Asp Asn Glu Gln Ala	Leu Asp Glu His Ile Arg Leu Ile Ala Glu	
530	535	540
Asp Ile Thr Lys Gly	Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val	
545	550	555
Ser Ser		

<210> 1639

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1639

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatgggtgca aagcgctctt gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgctttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1640

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1640

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1641
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1641

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatgggtgca	aagcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccactgt	atcacaaaagc	gggtgcgggc	cagaagctgc	cgctggcggg	tggtcgtgctg	360
ggatatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggtttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gtagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgca	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacctgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1642
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1642

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ser																

<210> 1643

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1643

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aagcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtagc aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttgg cagcgcggaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1644
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1644
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285

```

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290					295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1645

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1645

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcgc gcgcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1646
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1646
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```


				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
	275					280						285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290				295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420				425							430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470						475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1647
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcca aagcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattgggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgccca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1648
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1648
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35 40 45

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
50						55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120				125							
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
130						135				140							
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
		180					185					190					
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195					200					205						
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
210					215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230					235					240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245			250						255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
	275					280						285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
290					295					300							
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360					365						
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
370					375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405				410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
450					455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470				475						480		

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1649

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1649

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tggtgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcctgc	gttgccctgc	gcagtatacc	960
ggcccatttg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcggaac	1380
ctgaccgctc	gtagcattga	aatctttccag	tactatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaaggtggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1650
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1650

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1652
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1652
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500				505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1653

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1653

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60


```

agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccactgt atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag tactatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgcca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagggtggc cgtattgttc aggcgatcaa ccaagtggtt 1680
agcagt

```

<210> 1654

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1654

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Leu Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165				170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195				200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210				215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355				360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405				410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
4															

545
Ser Ser

550

555

560

<210> 1655
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1655
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag tactatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgcgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1656
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1656

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1657
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1657

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	agggtggccgc	tgttgcgctg	120
tatggtgcga	aagcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	gggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgctg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacgggtgcga	gcgggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttggt	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gtagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaagg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500

ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtggttgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgct	1620
ctgatcgagg	aggatatcac	caaaggtggc	cgtattgttc	aggcgatcaa	ccaagtgttt	1680
agcagt						1686

```
<210> 1658
<211> 562
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1658															
Met 1	Ile	Ile	Ala	Ser 5	Gln	Thr	Gln	Thr	Phe 10	Thr	Ser	Lys	Ser	Pro	His 15
Thr	Ala	Ser	Asp 20	Ser	Val	Val	Thr	Val 25	Gly	Asp	Lys	Pro	Leu 30	Thr	Ile
Asn	Glu	Val 35	Ala	Ala	Val	Ala	Arg 40	Tyr	Gly	Ala	Lys	Ala 45	Arg	Leu	Thr
Asp	Lys 50	Glu	Glu	Val	Leu	Gln 55	Arg	Val	Asn	Ala 60	Ser	Cys	Glu	Trp	Val
Ala 65	Gln	Ala	Val	Ala 70	Lys	Gly	Glu	Pro	Ile 75	Tyr	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn 100	Asn	Leu	Pro	Arg	Tyr	His 105	Lys	Ala	Gly	Ala 110	Gly	Gln	Lys
Leu	Pro 115	Leu	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu 125	Arg	Ala	Asn	Ser
His 130	Leu	His	Gly	Ala	Ser 135	Gly	Ile	Arg	Leu	Glu 140	Leu	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu
Glu	Met 195	Thr	Ala	Pro	Glu	Ala	Leu 200	Lys	Arg	Leu	Gly 205	Leu	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu 215	Gly	Leu	Ala	Met	Met 220	Asn	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala 230	Ala	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu 255	Asn	Gly
Thr	Asn	Gln 260	Ser	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro
Gly	Gln 275	Ile	Trp	Ser	Ala	Gln	Gln 280	Met	Leu	Glu	Leu 285	Leu	Gln	Gly	Ser
Gln	Leu 290	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His 300	Asp	Tyr	Arg	Gly	Glu
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu Lys
			405					410						415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
			420				425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440						445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Gln
	450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala Ile
		500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530					535					540			
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550					555					560
Ser	Ser													

<210> 1659
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1659
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgcgt aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgcga actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1660

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1660

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```


<210> 1661
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1661

```
atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccactgt atcacaaagc ggggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg gtagcattga aatcttcag tactatatg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1662

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1662

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Leu	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1664

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Gly	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1665

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1665

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tggtgcgctg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttgtag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1666
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1666
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccactgt atcacaaagc gggtgctgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaattttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag tactatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 1668

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1668

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Leu Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200		205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215		220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230		235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280		285
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295		300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310		315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345		350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360		365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375		380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390		395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425		430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440		445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455		460
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470		475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	500	505		510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520		525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535		540
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550		555
Ser	Ser																		560

<210> 1669
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1669
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcggc 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aagcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccattg cggacgggtat tgcagaaatc gcgaagcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttgc gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag tactatatgt cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgcc actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1670
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1670
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Gly Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

450		455		460	
Ser Ile Glu Ile Phe Gln Tyr Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 1671

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1671

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgag	ggcgtgaccc	cgacagtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggtggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgagggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccc	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacctgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 1672
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1672
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
 325 330 335

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390				395						400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420					425						430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
		500						505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515				520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1673

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1673

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgcga	aggcgctct	gaccgacaaa	gaggaagtgc	tcagcgctgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780

```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag tactatatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgct 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1674
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1674

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35				40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75				80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100					105						110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala	Leu Gln Gly Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His	Gln Cys Lys Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu	Glu Leu Leu Gln Gly Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser	His Asp Tyr Arg Gly Glu
290	295	300
Gln Pro Ile Gln Asp	Arg Tyr Ser Met Arg	Cys Leu Pro Gln Tyr Thr
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile	Ala Lys Gln Ile Glu Val
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu	Ile Asp Val Ala Gly Asn
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly	Gln Tyr Ile Gly Thr Ser
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu	Leu Ala Lys His Leu Asp
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu	Phe Asn Asn Gly Leu Pro
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Pro	Val Asn Met Gly Leu Lys
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met	Pro Leu Leu Thr Phe Tyr
420	425	430
Gly Asn Ser Leu Thr	Asp Arg Phe Pro Thr	His Ala Glu Gln Phe Asn
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser	Ala Asn Leu Thr Arg Arg
450	455	460
Ser Ile Glu Ile Phe	Gln Tyr Tyr Ile Ala	Ile Ala Leu Met Phe Gly
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys	Ile Ala Asn His Tyr Asp
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Cys	Gln Leu Tyr Leu Ala Ile
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys	Asp Arg Pro Tyr Ile Trp
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His	Ile Ala Leu Ile Ala Glu
530	535	540
Asp Ile Thr Lys Gly	Gly Arg Ile Val Gln	Ala Ile Asn Gln Val Val
545	550	555
Ser Ser		

<210> 1675

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1675

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aagcgctctt gaccgacaaa gaggaagtgc tgcagggtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcgga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgac agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 1676

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1676

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Gly Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405				410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515					520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1677
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1677

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatgggtg	gcgcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgcaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaaagc	gggtgcgggc	aaaaagctgc	cgctggcggg	tggtcgtg	360
ggatatgctgc	tgcggtgcgaa	cagccacctg	cacgggtgcga	gcgggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacg	ggcgtgaccc	cgacggtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	aaagcattga	aatcttccag	tactatatattg	cgatcgcgct	gatgttttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgcc	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1678
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1678

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Arg	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ser																

<210> 1679

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1679

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcggc 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aagcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccactgt atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcgaa cagccacctg caggtgcgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
agcatcggtg cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaaac 1380
ctgacccgtc gtagcattga aatcttccag tactatatgt cgatcgcgct gatgttttgt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1680
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1680
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Gly Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Leu Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225         230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245         250         255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260         265         270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275         280         285

```

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290					295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405				410						415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1681

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1681

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgcaagc gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tggttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcgca gcggtatccg tctggagctg 420

```



```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag tactatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1682
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1682
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```

				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260						265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340						345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420						425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475						480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1683

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aagcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgcaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgccagcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 1684
<211> 562
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1684

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
```

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Gln	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
450						455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1685

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1685

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtggttt	cgggtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgccaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccatttg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagccgcg	gcacctgtca	actgtatctg	gcgattaagg	aagtggttgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1686
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1686

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Ser	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg ctacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt
1686

```

<210> 1688
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1688
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```


Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310					315						320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345						350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355						360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370				375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390						395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420					425						430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450				455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530				535						540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550					555						560	
Ser	Ser															

<210> 1689

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1689

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
ctgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc cagaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1690

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1690

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Leu Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165				170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
4															

545
Ser Ser

550

555

560

<210> 1691
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1691
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgacccc ctggcgta caaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctg cgagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1692
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1692

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Ser	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1693

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1693

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggtctgccg 1200
gtagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500

```

<400> 1694															
Met 1	Ile	Ile	Ala	Ser 5	Gln	Thr	Gln	Thr	Phe 10	Thr	Ser	Lys	Ser	Pro	His 15
Thr	Ala	Ser	Asp 20	Ser	Val	Val	Thr	Val 25	Gly	Asp	Lys	Pro	Leu 30	Thr	Ile
Asn	Glu	Val 35	Ala	Ala	Val	Ala	Arg 40	Tyr	Gly	Ala	Lys	Ala 45	Arg	Leu	Thr
Asp	Lys 50	Glu	Glu	Val	Leu	Gln 55	Arg	Val	Asn	Ala	Ser 60	Cys	Glu	Trp	Val
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn 100	Asn	Leu	Pro	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg 125	Ala	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu	Leu 140	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala	Leu	Lys 200	Leu	Leu	Gly	Leu	Glu	Pro	Leu
Glu	Leu 210	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn	Gly 255
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Gln	Leu 290	Ile	Arg	Asp	Glu	Leu	Asp 295	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu Lys
			405					410						415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
		420				425							430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440						445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Arg
	450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala Ile
		500				505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520						525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Arg	Leu	Ile	Ala Glu
	530				535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550					555					560
Ser	Ser													

<210> 1695

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1695

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
aatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```



```

aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1696

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1696

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Asn Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```

<210> 1697
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1697

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgccgct 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgta atagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1698

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1698

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195					200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Asn
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1700

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Leu	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1701

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1701

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	agggtggccgc	tggttgcgcgt	120
catggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccggtgc	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgtag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1702
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1702
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg His Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc cagaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgtc actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 1704

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1704

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Lys Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ser																		

<210> 1705
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1705
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa catgaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1706
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1706
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	His	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Cys Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 1707

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1707

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgcca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcaciaaagc	gggtgctggc	cagaagctgc	cgctggcgga	tgcttctgctg	360
ggatatgctgc	tgcgtgcaaa	cagccacctg	cacgggtgca	gcggatatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgag	ggcgtgaccc	cgacagcttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggtggg	540
ctgaacgaca	gttataaccg	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgga	tgatgaccgg	tattgctggc	aactgcgttt	atgatgcaac	gaacctgctg	720
gcgctgagcc	tgggtgcaac	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccc	caccgggggc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgctggc	aagagccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacgggat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgct	ggtaacgcga	gctaccacgg	tggaacttcc	1080
atgggccaagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccc	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaaagc	ttgacctgca	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacctgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgca	1620
ctgatcgagg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 1708

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1708

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
          290          295          300
Glu Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305          310          315          320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
          325          330          335

```

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
		500						505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ser															

<210> 1709

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1709

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgcga	aggcgtctct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaca	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780


```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggccccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1710

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1710

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Ser Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala Leu Gln Gly	Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His Gln Cys Lys	Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu Glu Leu Leu Gln Gly	Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser His Asp Tyr Arg Gly	Glu
290	295	300
Gln Pro Ile Gln Asp	Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr	
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val	
325	330	335
Glu Ile Asn Ser Val Thr	Asp Asn Pro Leu Ile Asp Val Ala Gly Asn	
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser	
355	360	365
Met Asp Arg Leu Arg Tyr	Tyr Leu Gly Leu Leu Ala Lys His Leu Asp	
370	375	380
Val Gln Ile Ala Leu Leu Thr	Met Pro Glu Phe Asn Asn Gly Leu Pro	
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys	
405	410	415
Gly Leu Gln Ile Thr Gly	Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr	
420	425	430
Gly Asn Ser Leu Thr Asp	Arg Phe Pro Thr His Ala Glu Gln Phe Asn	
435	440	445
Gln Asn Ile Asn Ser Gln	Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg	
450	455	460
Ser Ile Glu Ile Phe Gln	Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly	
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp	
485	490	495
Ala Ser Gln Cys Leu Ser	Pro Arg Thr Cys Gln Leu Tyr Leu Ala Ile	
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp	
515	520	525
Asn Asp Asn Glu Gln Ala	Leu Asp Glu His Ile Ala Leu Ile Ala Glu	
530	535	540
Asp Ile Thr Lys Gly	Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val	
545	550	555
Ser Ser		

<210> 1711

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1711

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacagtagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggcgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1712

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1712

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85           90           95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515					520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1713
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1713
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
 tatgggtgcgg aggcgctctt gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtt taccactggg 240
 ttcggttggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
 agcatcggtg cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctggttggg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
 accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
 ccgaccacg cgagcagttt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
 ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1714
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1714

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Glu	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ser																

<210> 1715

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1715

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgctctt gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgactgc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1716
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1716
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50           55           60
Ala Thr Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
275          280          285

```


Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1717

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1717

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta aggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcgca gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1718
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1718
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Lys Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```


<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1719

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 1720
<211> 562
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1720

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
```

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
50						55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
130						135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
210						215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
290						295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
370						375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390						395				400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1721

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1721

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcgt	120
agtgggtgca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacctgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1722
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1722

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Ser	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1724
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1724
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Arg Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1725

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1725

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
cagggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc cagaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1726

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1726

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Gln Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165				170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195				200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210				215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230					235						240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245			250						255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355				360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405				410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
4															

545
Ser Ser

550

555

560

<210> 1727
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1727
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct ggccggacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgcaagc ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggc cagaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggg tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaac cagaccgtcc gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagc ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1728
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1728

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Ala
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1729

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1729

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500

```

```

ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaacatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1730
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1730
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr

```


305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu Lys
			405					410						415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
			420				425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440						445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Arg
	450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala Ile
		500				505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	His	Arg	Pro	Tyr	Ile Trp
	515					520						525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530				535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550					555					560
Ser	Ser													

<210> 1731
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1731
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgaatgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgcgt gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1732
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1732
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190

```

<210>	1733
<211>	1686
<212>	DNA
<213>	Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1733

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtctgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1734

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1734

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1736

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Asn	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340					345						350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1737

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1737

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	agggtggccgc	tggttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacatg	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccgggtgc	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140


```

aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1738
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1738
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Met Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc cagaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 1740
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1740
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Ser Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ser																		

<210> 1741
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1741
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgacgcttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggtggg 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacgggtat tgctgaaatc gcgaagcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtgggtgg taagccgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1742
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1742
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Cys Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Pro Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 1743

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1743

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgcca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcaciaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacgggtcga	gcggatatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacagtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggtggg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgga	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgagggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcggaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacctgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaggagccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 1744

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1744

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
      325     330     335

```


Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390				395						400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
		500						505					510			
Lys	Glu	Val	Val	Gly	Lys	Glu	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1745

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1745

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggttc	caagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780

```

ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1746

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1746

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Ser Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala Leu Gln Gly	Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His Gln Cys Lys	Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu Glu Leu Leu Gln Gly	Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser His Asp Tyr Arg Gly	Glu
290	295	300
Gln Pro Ile Gln Asp	Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr	
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val	
325	330	335
Glu Ile Asn Ser Val Thr	Asp Asn Pro Leu Ile Asp Val Ala Gly Asn	
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser	
355	360	365
Met Asp Arg Leu Arg Tyr	Tyr Leu Gly Leu Leu Ala Lys His Leu Asp	
370	375	380
Val Gln Ile Ala Leu Leu Thr	Met Pro Glu Phe Asn Asn Gly Leu Pro	
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys	
405	410	415
Gly Leu Gln Ile Thr Gly	Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr	
420	425	430
Gly Asn Ser Leu Thr Asp	Arg Phe Pro Thr His Ala Glu Gln Phe Asn	
435	440	445
Gln Asn Ile Asn Ser Gln	Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg	
450	455	460
Ser Ile Glu Ile Phe Gln	Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly	
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp	
485	490	495
Ala Ser Gln Cys Leu Ser	Pro Arg Thr Cys Gln Leu Tyr Leu Ala Ile	
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp	
515	520	525
Asn Asp Asn Glu Gln Ala	Leu Asp Glu His Ile Ala Leu Ile Ala Glu	
530	535	540
Asp Ile Thr Lys Gly	Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val	
545	550	555
Ser Ser		

<210> 1747

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1747

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ctgtgggtga taagccgctg acgatcaatg aggtgacggc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggcgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 1748

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1748

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Thr Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515					520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1749
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1749

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatgggtgca	aggcgctctt	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggttggc	tggcgcaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcggg	tggtcgtgctg	360
ggatatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgctaca	tcaccgggtg	gctgggttggt	540
ctgaacgaca	gttataacct	tgatttttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaa	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatctttccag	caatatattg	cgatcgcgct	gatgttttggt	1440
gtgcaaagcg	ttgacctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacctgtca	actgtatctg	gcgattaagg	aagtgggttg	taagaagccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattg	1620
ctgatcgcg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1750
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1750

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485				490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Lys	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515						520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550				555						560		
Ser	Ser																

<210> 1751

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1751

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatgggtgcgc ctgcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggc 240
ttcggtaggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggc 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtac caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320

```



```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1752
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1752
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Pro Ala Arg Leu Thr
35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
275          280          285

```

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1753

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1753

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggttg aggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtgcca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1754
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1754
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Glu Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```


<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1755

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgcaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc ggggtgcggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg ttcggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 1756
<211> 562
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1756

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
```

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
50						55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120				125							
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
130						135				140							
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
210						215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230					235					240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265					270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
	275						280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
290						295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
370						375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
450						455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470				475						480		

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Ser	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1757

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1757

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tggtgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcggaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaactt	1500
ctgagcccgc	gcacctgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1758
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1758

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1760
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1760
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Gly
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1761
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1761
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc cagaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcccgg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgcgt gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattcat 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1762

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1762

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165				170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230					235						240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330				335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410				415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
4															

545
Ser Ser

550

555

560

<210> 1763
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1763
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggc cagaagctgc cgctggcggg tgttcgtgctg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaac cagaccgtcc gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatcac caaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1764
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1764

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Met
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1765
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1765

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	agggtggccgc	tgttgcgcgct	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcgtgc	ggttgcgaag	gggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcggga	tgttcgtgcg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttggt	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gtagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500


```

ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat acggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgaggatatacac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 1766
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1766
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala His Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr

```

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu Lys
			405					410						415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
		420				425							430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440						445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Arg
	450				455						460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala Ile
		500				505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Arg
	515					520						525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530				535						540			
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550				555						560
Ser	Ser													

<210> 1767
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1767
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacct gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg gaaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1768

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1768

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```

<210> 1769
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1769

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgccgct 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggg cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgca gcacctgtca actgtatctg gcgattaagg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1770

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1770

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
	195					200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1772

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Ala	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 1773

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1773

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtggttc	aggtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1774
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1774
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Gln Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc cagaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgacccc cgcacgtttg cgaattttggt 480
agcatcgggtg cgagcgggtga cctgaccccc ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 1776

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1776

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Ala Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200		205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215		220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230		235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280		285
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295		300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310		315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345		350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360		365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375		380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390		395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425		430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440		445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455		460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470		475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	500	505		510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520		525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535		540
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550		555
Ser	Ser																		

<210> 1777
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1777
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgtctcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgctgaaatc gcgaagcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1778
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1778
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Ser	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Cys Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 1779

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1779

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgca	aggcgcgtct	gaccgacaaa	gctgaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcaciaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacgggtgcg	gcggatatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacagtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggtggg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgagggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacctgtca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 1780

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1780

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Ala Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
      325     330     335

```

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390				395						400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
		500						505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1781

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1781

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcggg ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```

```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggccccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1782

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1782

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Val Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala Leu Gln Gly	Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His Gln Cys Lys	Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu Glu Leu Leu Gln Gly	Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser His Asp Tyr Arg Gly	Glu
290	295	300
Gln Pro Ile Gln Asp	Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr	
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val	
325	330	335
Glu Ile Asn Ser Val Thr	Asp Asn Pro Leu Ile Asp Val Ala Gly Asn	
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser	
355	360	365
Met Asp Arg Leu Arg Tyr	Tyr Leu Gly Leu Leu Ala Lys His Leu Asp	
370	375	380
Val Gln Ile Ala Leu Leu Thr	Met Pro Glu Phe Asn Asn Gly Leu Pro	
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys	
405	410	415
Gly Leu Gln Ile Thr Gly	Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr	
420	425	430
Gly Asn Ser Leu Thr Asp	Arg Phe Pro Thr His Ala Glu Gln Phe Asn	
435	440	445
Gln Asn Ile Asn Ser Gln	Gly Phe Gly Ser Ala Asn Leu Thr Arg Arg	
450	455	460
Ser Ile Glu Ile Phe Gln	Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly	
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp	
485	490	495
Ala Ser Gln Cys Leu Ser	Pro Arg Thr Cys Gln Leu Tyr Leu Ala Ile	
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp	
515	520	525
Asn Asp Asn Glu Gln Ala	Leu Asp Glu His Ile Ala Leu Ile Ala Glu	
530	535	540
Asp Ile Thr Lys Gly	Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val	
545	550	555
Ser Ser		

<210> 1783

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1783

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ctgtgggtga taagccgctg acgatcgagg aggtggccgc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1784

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1784

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Glu Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1785
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1785

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatgggtgca	aggcgctctt	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tggtcgtgctg	360
ggatatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttggt	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgtggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacctcg	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgctg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacctgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcg	aggatatcat	gaaaggcggc	cgtattattc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1786
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1786

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Met	Lys	Gly	Gly	Arg	Ile	Ile	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ser																

<210> 1787

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1787

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtagga tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg cagcggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttgg cagcgcgaaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1788
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1788
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225         230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245         250         255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Ala
          260         265         270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275         280         285

```

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1789

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1789

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gggaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtag cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1790
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1790
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```

				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
	275					280						285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
290					295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Gly	Lys	Gln	Ile	Glu	Val		
			325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360					365						
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
370					375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420				425						430					
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
450					455					460							
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490					495				
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505					510					
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
530					535					540							
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550					555						560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1791
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtag cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcactg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1792
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1792
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35 40 45

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Thr	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1793

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1793

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccatttg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	gtagcattga	aatctttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacctgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgtgg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1794
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1794

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgcttaa ccaagtgggt 1680
agcagt
1686

```

<210> 1796
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1796
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325					330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340					345						350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355						360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Leu	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1797

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1797

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc cagaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcccgg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caaccaaaac atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc agagtatcaa ccaagtgggt 1680
agcagt

```

<210> 1798

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1798

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165				170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195				200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210				215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345						350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355				360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405				410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450				455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
4															

545
Ser Ser

550

555

560

<210> 1799
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1799
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc gtagcattga aatcttcatt caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1800
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1800

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Ile	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1801

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1801

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500

```

```

ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaatatgtt 1680
agcagt 1686

```

<210> 1802
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1802
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr

```

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu Lys
			405					410						415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
			420				425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440						445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Arg
	450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala Ile
		500				505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520						525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530				535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Tyr Val
545				550				555						560
Ser	Ser													

<210> 1803
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1803
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccttctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1804

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1804

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```

<210>	1805
<211>	1686
<212>	DNA
<213>	Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1805

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgccgct 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg gtagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1806

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1806

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1808

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Leu	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Ser	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1809

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1809

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tggtgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccggtgc	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgtggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccgt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgtag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttcacg caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

```

<210> 1810
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 1810
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc cagaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg cagggctgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaattttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgctg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttccttggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggtttttg cagcgcgaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1812
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1812
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ser																		

<210> 1813
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1813
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
agcatcggtg cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acacgctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1814
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1814
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Cys Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Gly Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 1815

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1815

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgcca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgctggc	cagaagctgc	cgctggcgga	tgcttctgctg	360
ggatatgctgc	tgcgtgcaaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgag	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccggtgc	gctgggtggg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcaaa	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaacgg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgagggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccc	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaaagc	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcaccgagca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 1816

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1816

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
      325     330     335

```



```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaatgtgtt 1680
agcagt 1686

```

<210> 1818

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1818

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala	Leu Gln Gly Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His	Gln Cys Lys Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu	Glu Leu Leu Gln Gly Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser	His Asp Tyr Arg Gly Glu
290	295	300
Gln Pro Ile Gln Asp	Arg Tyr Ser Met Arg	Cys Leu Pro Gln Tyr Thr
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile	Ala Lys Gln Ile Glu Val
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu	Ile Asp Val Ala Gly Asn
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly	Gln Tyr Ile Gly Thr Ser
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu	Leu Ala Lys His Leu Asp
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu	Phe Asn Asn Gly Leu Pro
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Pro	Val Asn Met Gly Leu Lys
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met	Pro Leu Leu Thr Phe Tyr
420	425	430
Gly Asn Ser Leu Thr	Asp Arg Phe Pro Thr	His Ala Glu Gln Phe Asn
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser	Ala Asn Leu Thr Arg Arg
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala	Ile Ala Leu Met Phe Gly
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys	Ile Ala Asn His Tyr Asp
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Cys	Gln Leu Tyr Leu Ala Ile
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys	Asp Arg Pro Tyr Ile Trp
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His	Ile Ala Leu Ile Ala Glu
530	535	540
Asp Ile Thr Lys Gly	Gly Arg Ile Val Gln	Ala Ile Asn Gln Cys Val
545	550	555
Ser Ser		

<210> 1819

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1819

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggcgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcggtgaa ccaagtgggt 1680
agcagt 1686
```

<210> 1820

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1820

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Val	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1821
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1821
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatgggtgca aggcgctctt gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggc tggcgcaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcggg tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggg 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
 gctagcctgg tgggtaacac cgaccgtccg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
 ccgaccacg cgagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
 ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
 ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaaattgtt 1680
 agcagt 1686

<210> 1822
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1822

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Ile	Val		
545					550					555					560		
Ser	Ser																

<210> 1823

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1823

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggttggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgctttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttgg cagcgcggaac 1380
ctgacccgtc gtagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaacatgtt 1680
agcagt
1686

```

<210> 1824
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1824
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
275          280          285

```

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	His	Val
545					550					555					560
Ser	Ser														

<210> 1825

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1825

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc cagaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcgca gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattgggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacctgtca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaaatggtt 1680
agcagt
1686

```

<210> 1826
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1826
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```

				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
	275					280						285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
290					295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
370					375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420				425							430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg		
450					455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470						475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Met	Val		
545				550						555					560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1827
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgcaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggca tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc ggggtgcggc cagaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta taccgggtgc gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcactggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1828
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1828
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35 40 45

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Thr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg	
450						455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1829

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1829

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	cagaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaactgctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccatttg	cggacggtat	tgctgaaatc	gcgaagcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	ggtaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcggaac	1380
ctgaccgctc	gtagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacctgtca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaaggcggc	cgtattgttc	aggcgatcaa	ccaacttggt	1680
agcagt						1686

<210> 1830
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1830

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215						220			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacctgca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaatatgtt 1680
agcagt
1686

```

<210> 1832
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1832
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Leu Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Cys	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325					330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340						345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355						360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Tyr	Val
545					550					555					560
Ser	Ser														

<210> 1833
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1833
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc cagaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgctgaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acgctctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacctgtca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaaggcggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1834
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1834
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

	115						120						125					
His 130	Leu	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu	Leu 140	Ile	Gln	Arg	Ile			
Glu 145	Thr	Phe	Leu	Asn 150	Ala	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160			
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175			
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr	Thr 185	Val	Asp	Phe	Asn	Gly	Glu			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu			
Glu	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val			
Met 225	Thr	Gly	Ile	Ala	Ala	Asn 230	Cys	Val	Tyr	Asp	Ala 235	Gln	Asn	Leu	Leu 240			
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly 255			
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile	His 265	Gln	Cys	Lys	Pro	His	Pro			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu			
Gln 305	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu 315	Pro	Gln	Tyr	Thr 320			
Gly	Pro	Ile	Ala	Asp 325	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val 335			
Glu	Ile	Asn	Ser 340	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn 350			
Ala	Ser	Tyr	His 355	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser 365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr 375	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp 380			
Val 385	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro 400			
Ala	Ser	Leu	Val	Gly 405	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys 415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr 430			
Gly	Asn	Ala	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn 445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly 455	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg 460			
Ser 465	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly 480			
Val	Gln	Ser	Val	Asp 485	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp 495			
Ala	Ser	Gln	Cys 500	Leu	Ser	Pro	Arg	Thr	Cys	Gln	Leu	Tyr	Leu	Ala	Ile 510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp 525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu 540			
Asp	Ile	Thr	Lys	Gly	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val 550			

545
Ser Ser

550

555

560

<210> 1835
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1835
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcggg tgaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1836
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1836

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Val	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1837

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1837

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaagctgc cgctggcggc tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttag cagcgcaaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaactg 1500

```

```

ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgaggatatacac caaagatggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 1838
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1838
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145      150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225      230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr

```

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu Lys
			405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
		420				425							430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Ser	Ser	Ala	Asn	Leu	Thr	Arg Gln
	450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490					495	
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala Ile
		500				505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530				535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550				555						560
Ser	Ser													

<210> 1839

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1839

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgagccgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacct gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggc tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc agaggcgctg 600

```

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgcga actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1840

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1840

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Ser Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1841

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtaggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcggt tgaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tcatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtcgtt 1680
agcagt
```

<210> 1842

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1842

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Val	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1844

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1845

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1845

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	agggtgcggc	tggttgcgct	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccc	ctggcgtaca	tcaccgggtg	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	agaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttgtag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgcagaaatc	gcgaaacaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgtttcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtcgtt 1680
agcagt
1686

```

<210> 1846
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1846
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcggg tgaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgccca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaaatcgtt 1686
agcagt

```

<210> 1848

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1848

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Val	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425	430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Ile	Val	545	550	555	560
Ser	Ser																		

<210> 1849
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1849
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggtggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc agaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1850
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1850
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 1851

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1851

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggcggc	tgttgcgctg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacgggtcga	gcggatatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcgtaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	agaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcagaaatc	gcgaaacaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtcct	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 1852
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1852
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
 325 330 335

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390				395						400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410						415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1853

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1853

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaacgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcggg tgaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggataccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```

```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttag cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cccccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgag 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1854
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1854
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Val Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala	Leu Gln Gly Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His	Gln Cys Lys Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu	Glu Leu Leu Gln Gly Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser	His Asp Tyr Arg Gly Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg	Cys Leu Pro Gln Tyr Thr
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile	Ala Asn Gln Ile Glu Val
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu	Ile Asp Val Ala Gly Asn
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly	Gln Tyr Ile Gly Thr Ser
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu	Leu Ala Lys His Leu Asp
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu	Phe Asn Asn Gly Leu Pro
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Pro	Val Asn Met Gly Leu Lys
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met	Pro Leu Leu Thr Phe Tyr
420	425	430
Gly Asn Ser Leu Thr	Asp Arg Phe Pro Thr	His Ala Glu Gln Phe Asn
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Ser Ser	Ala Asn Leu Thr Arg Gln
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala	Ile Ala Leu Met Phe Gly
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys	Ile Ala Asn His Tyr Asp
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Arg	Gln Leu Tyr Leu Ala Ile
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys	Asp Arg Pro Tyr Ile Trp
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His	Ile Ala Leu Ile Ala Glu
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln	Ala Ile Asn Gln Val Val
545	550	555
Ser Ser		

<210> 1855

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1855

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgagccgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggcgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc agaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggtttag cagcgcgaa 1380
ctgaccctg aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgtcg aggatatcgg caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1856

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1856

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Ser Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Ser	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Val	Glu
530						535					540				
Asp	Ile	Gly	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1857
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1857
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
 tatgggtgca aggcgctctt gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgaacgc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
 agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc agaggcgctg 600
 aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
 gctagcctgg tgggtaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
 accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
 ccgaccacg cgagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
 ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgc gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
 ctgatcgctg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1858
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1858

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Asn	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys

				405					410					415					
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr				
			420					425					430						
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn				
		435					440					445							
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln				
	450					455					460								
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly				
465					470				475						480				
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp				
			485					490						495					
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile				
		500						505					510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp				
	515					520						525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545					550				555						560				
Ser	Ser																		

<210> 1859

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1859

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgtggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcggt tgaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccagcag 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaaacaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttcg gggaaacgca gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgc gcacccgcca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtggtt 1680
agcagt
1686

```

<210> 1860
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1860
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180          185          190
Glu Met Thr Ala Val Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
275          280          285

```

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1861

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1861

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc agaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaaacaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgtcg aggatatcgg caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1862
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1862
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```

				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
	275					280						285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290				295						300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420				425							430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470						475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Val	Glu		
	530				535						540						
Asp	Ile	Gly	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1863
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagagg ggttgcggaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc ggggtgcggc caaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttacatagg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccgc gcaccgccca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1864
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1864
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35 40 45

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
50						55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
130						135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
210						215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
290						295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340						345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
370						375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
450						455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1865

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1865

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggcggc	tggtgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttggg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcggg	tgaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccatttg	cggacgggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtcct	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	aaagcattga	aatctttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgcc	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1866
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1866

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Val	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgcgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1868
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1868
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Val Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1869

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1869

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcggg tgaggcgcgt 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgcgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1870
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1870
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Val	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210				215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345						350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450				455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
4															

545
Ser Ser

550

555

560

<210> 1871
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1871
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaacgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtgc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1872
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1872

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Asn	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500						505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1873

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1873

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcggt tgaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500

```

```

ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt                                           1686

```

<210> 1874
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1874
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Val Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
      290     295     300
Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr

```

305					310					315				320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420				425							430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500				505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ser														

<210> 1875

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1875

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacct gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggc caaaagctgc cgctggcggc tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacgggat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgcga actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1876

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1876

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1877

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcggt tgaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtcct gttacatagg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1878

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1878

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```


65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
				100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
				115					120					125		
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
				130					135					140		
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
				180					185					190		
Glu	Met	Thr	Ala	Val	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
				195					200					205		
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
				210					215					220		
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
				260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
				275					280					285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
				290					295					300		
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
				340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
				355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
				370					375					380		
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
				420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
				435					440					445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
				450					455					460		
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg										

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1880

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1881

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1881

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tggtgcgctg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgaacgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	agaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgtag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1882
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1882
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Asn Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc agaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg caccgccca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaaatcgtt 1686
agcagt

```

<210> 1884
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1884
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Ser Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200		205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215		220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230		235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280		285
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295		300
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310		315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345		350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360		365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375		380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390		395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425		430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440		445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455		460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470		475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505		510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520		525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535		540
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Ile	Val	545	550		555
Ser	Ser																		560

<210> 1885
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1885
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc agaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gctgtagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacgggtac caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccc caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagccgc gcaccgccca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1886
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1886
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Leu Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 1887

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1887

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggcggc	tgttgcgctg	120
tatggtgcca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tgcttcgtgc	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgacagtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcggg	tgaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgagggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccc	1200
gctagcctgg	tgggtaaacac	cgaccgtatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 1888

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1888

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Val Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val
      325     330     335

```

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1889

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1889

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcaaa cagccacctg cacgggtgca gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```

```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggccccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cccccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1890
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1890

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35				40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75				80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100					105						110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155				160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
	195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala Leu Gln Gly	Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His Gln Cys Lys	Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu Glu Leu Leu Gln Gly	Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser His Asp Tyr Arg Gly	Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr	
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val	
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn	
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser	
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp	
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro	
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Met Val Asn Met Gly Leu Lys	
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr	
420	425	430
Gly Asn Ser Leu Thr	Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn	
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Gln	
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly	
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp	
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile	
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp	
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu	
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val	
545	550	555
Ser Ser		

<210> 1891

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1891

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggtggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcggc tgaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacac cgaccgtatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1892

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1892

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```


Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Val	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
				325				330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515				520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1893
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1893

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tggtgcgcgt	120
tatgggtgca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgagccgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tggtcgtgcg	360
ggatatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggtttg	cgaatttggt	480
agcatcggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggaaccttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaa	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgttttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgc	gcacccgcca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1894
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1894

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Ser	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550				555						560		
Ser	Ser																

<210> 1895

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1895

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgtggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacccgccca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1896
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1896
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285

```

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290					295						300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1897

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1897

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcggt tgaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgac agctggatgg tagccacgac 900
taccgcgcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgtcg aggatatcgg caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1898
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1898
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```

				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Val	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275				280						285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420				425							430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470						475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Val	Glu		
	530				535						540						
Asp	Ile	Gly	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1899

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatggtgcca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaacgc ggttgccaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc ggggtgcggc caaagctgc cgctggcggg tgcttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaaacaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtag cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgccca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 1900
<211> 562
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1900

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
```

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Asn	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
450						455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1901

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1901

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tggttcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgaacgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccatttg	cggacgggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcggaac	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccg	gcacccgcc	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1902
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1902

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Asn	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100					105						110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgcagaaatc gcgaaacaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1904
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1904
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Val Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500						505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1905

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1905

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcgt gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcgg tgatgaccgg tattgcccgg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgcgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1906

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1906

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```


[illegible]

545
Ser Ser

550

555

560

<210> 1907
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1907
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggc tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc agaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc aggggttttag cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatcac caaagatggc cgtattgttc agtcgatcaa ccaagtcgtt 1680
agcagt 1686

<210> 1908
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1908

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His			
1				5					10					15				
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile			
			20					25					30					
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr			
		35					40					45						
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val			
	50					55					60							
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly			
65					70					75					80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu			
				85					90					95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys			
			100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser			
		115					120					125						
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile			
	130					135						140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly			
145					150					155					160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly			
				165					170					175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu			
			180					185					190					
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu			
		195					200					205						
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
		210				215					220							
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu			
225					230					235					240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly			
				245					250					255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro			
			260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser			
		275					280						285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu			
	290					295					300							
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr			
305					310					315					320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val			
				325					330					335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn			
			340					345					350					
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser			
		355					360					365						
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp			
	370					375					380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro			
385					390					395					400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys			
				405					410					415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr			
			420					425					430					

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Ser	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1909

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1909

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacct gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc agaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtcct gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttag cagcgcaaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500

```

ctgagcccg	gcacccgca	actgtatctg	gcgattaagg	aagtggttgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattg	1620
ctgatcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgtt	1680
agcagt						1686

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu Lys
			405					410						415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
			420				425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440						445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Ser	Ser	Ala	Asn	Leu	Thr	Arg Gln
	450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala Ile
		500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530					535				540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550					555					560
Ser	Ser													

<210> 1911
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1911
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggc tggcgaaact gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg cacgcgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacgggat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtacaa gcatcatgcc gctgctgacc ttctacggca acacgctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgcga actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgctgat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1912
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1912
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
           20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
           35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
           50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
           85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
           100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
           115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
           130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
           165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
           180          185          190

```

<210> 1913
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1913

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg cacgcgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cgagcggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca actcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1914

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1914

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
				100					105					110	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
				115					120					125	
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
				130					135					140	
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
				145					150					155	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
				225					230					235	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Ala
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
				305					310					315	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
				385					390					395	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
				465					470					475	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His		

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1916

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Ser	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185						190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Ala
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375						380			

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Leu	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
		530					535					540			
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1917

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1917

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tggtgcgctg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgca	tgctgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccg	ttattcacca	gtgcaaaccg	cacgcgggtc	aaatttgagg	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca actcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag tactatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcaccg 1560
agcaaagatc gtccgctgat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1918
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1918
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Ala

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgctttg cgaatttggt 480
agcatcggtg cgagcggtag cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca actcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcc actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 1920
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1920
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```


Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met	195	200		205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215		220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230		235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280		285
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295		300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310		315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345		350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360		365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375		380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390		395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425		430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440		445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455		460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470		475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505		510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520		525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535		540
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550		555
Ser	Ser																		

<210> 1921
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1921
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgag ggctgaccc cgacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccc cagcggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcaccggca acacgctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaggcaccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1922
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1922
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Ala
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Thr
			420				425				430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 1923

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1923

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgctggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggcgtgacct cgacgctttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccggtgc gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaac tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcttgggca actcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcacccgcca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgctgat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680

```

<210> 1924
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1924
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
 325 330 335

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390				395						400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Leu	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1925

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1925

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcggc	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcgggtga	cctgaccccg	ctggcgtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcggt	tgaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtac	caaccagagc	780

```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggccccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcaccggca actcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgcgcca actgtatctg gcgattaagg aagtgggttg taagaagccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgac 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1926
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1926

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Gly	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35				40						45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75				80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100					105						110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Val	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala Leu Gln Gly	Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His Gln Cys Lys	Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu Glu Leu Leu Gln Gly	Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser His Asp Tyr Arg Gly	Glu
290	295	300
Gln Pro Ile Gln Asp	Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr	
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val	
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn	
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser	
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp	
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro	
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Pro Val Asn Met Gly Leu Lys	
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Thr	
420	425	430
Gly Asn Ser Leu Thr	Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn	
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Gln	
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly	
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp	
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile	
500	505	510
Lys Glu Val Val Gly	Lys Lys Pro Ser Lys Asp Arg Pro Tyr Ile Trp	
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu	
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val	
545	550	555
Ser Ser		

<210> 1927

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1927

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tacgggtgcgg aggcgagcct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggcgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaacgcctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgcgcg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 1928

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1928

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Glu Ala Ser Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405				410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515					520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1929
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1929

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	agggtggccgc	tgttgccgct	120
tatgggtgca	aggcgctct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaaagc	gggtgcgggc	aaaaagctgc	cgctggcggg	tggtcgtgctg	360
ggatatgctgc	tgctgtcgaa	cagccacctg	cacgggtgcga	gcgggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgatttttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacctcg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaa	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gtagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgttttgg	1440
gtgcaaagcg	ttgacctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgcca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgctgat	ctggaacgac	aacgagcagg	cgctggatga	acacattg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1930
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1930

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Leu	Ile	Trp		
	515					520					525						
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ser																

<210> 1931

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1931

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc agggtttttg cagcgcgaaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacccgcca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtggtt 1680
agcagt
1686

```

<210> 1932
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1932

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245						250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1933

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1933

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcgga gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acacgctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgccca actgtatctg gcgattaagg aagtgggttg taaggcaccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1934
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1934
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```


				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
	275					280						285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420				425							430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470						475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1935
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag tactatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcaccgcca actgtatctg gcgattaagg aagtgggttg taaggcaccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1936
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1936
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35 40 45

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
50						55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115				120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
130						135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
210						215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
290						295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
370						375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390						395				400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
450						455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1937

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1937

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tggtgcgcgt	120
tacggtgcga	aggcgagcct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	gctgctgacc	ttcctgggca	actcgtgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	aaagcattga	aatcttccag	tactatattg	cgatcgcgct	gatgttttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccg	gcacccgcc	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1938
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1938

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Ser	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcaccggca actcgtctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgcgcca actgtatctg gcgattaagg aagtgggttg taagaagccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1940
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1940
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Glu Ala Ser Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Thr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Lys	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1941
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1941
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60


```

agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc aaaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg cacgcgggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcaagcaaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaac gcatcatgcc gctgctgacc ttctacggca actcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgccca actgtatctg gcgattaagg aagtgggtgg taagaagccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1942

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1942

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210				215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Ala
			260				265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345						350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450				455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
4															

545
Ser Ser

550

555

560

<210> 1943
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1943
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acacgctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgcca actgtatctg gcgattaagg aagtgggttg taaggcaccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatcac caagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1944
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1944

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		

Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500						505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1945

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1945

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
ctgggtgcga aggcgcgcct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcaagcaaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttaccggca actcgctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500

```

ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtggttgg	taaggcgccg	1560
agcaaagatc	gtccgctgat	ctggaacgac	aacgagcagg	cgctggatga	acacattg	1620
ctgatcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgtt	1680
agcagt						1686

```
<210> 1946
<211> 562
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1946															
Met 1	Ile	Ile	Ala	Ser 5	Gln	Thr	Gln	Thr	Phe 10	Thr	Ser	Lys	Ser	Pro 15	His
Thr	Ala	Ser	Asp 20	Ser	Val	Val	Thr	Val 25	Gly	Asp	Lys	Pro 30	Leu	Thr	Ile
Asn	Glu	Val 35	Ala	Ala	Val	Ala	Arg 40	Leu	Gly	Ala	Lys	Ala 45	Arg	Leu	Thr
Asp	Lys 50	Glu	Glu	Val	Leu	Gln 55	Arg	Val	Asn	Ala	Ser 60	Cys	Glu	Trp	Val
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn 100	Asn	Leu	Pro	Arg	Tyr	His 105	Lys	Ala	Gly	Ala 110	Gly	Gln	Lys
Leu	Pro 115	Leu	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu 125	Arg	Ala	Asn	Ser
His 130	Leu	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu	Leu 140	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val 180	Gly	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu
Glu	Met 195	Thr	Ala	Pro	Glu	Ala	Leu 200	Lys	Arg	Leu	Gly	Leu 205	Glu	Pro	Leu
Glu 210	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu 255	Asn	Gly
Thr	Asn	Gln 260	Ser	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro 270	His	Pro
Gly	Gln 275	Ile	Trp	Ser	Ala	Gln	Gln 280	Met	Leu	Glu	Leu	Leu 285	Gln	Gly	Ser
Gln	Leu 290	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr

305					310					315				320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Thr
		420				425							430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500				505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Leu	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ser														

<210> 1947
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1947
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtggttg aagtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tacggtgcca aggcgagcct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcaagc ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acacgctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgcga actgtatctg gcgattaagg aagtggttgg ttcggcaccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1948

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1948

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Glu Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Ser Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190

```


<210> 1949
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1949

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcggc 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgccgct 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggg caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtggttgg taaggcgcg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1950

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1950

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Gly Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
				100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
				115					120					125		
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
				130					135					140		
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
				180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
				195					200					205		
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
				210					215					220		
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
				260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
				275					280					285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
				290					295					300		
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
				340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
				355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
				370					375					380		
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
				420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
				435					440					445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
				450					455					460		
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg										

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1952

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Lys	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1953

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1953

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	agggtggccgc	tggttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccggtgc	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccgt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgtag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acacgctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtggttg taagaagccg 1560
agcaaagatc gtccgctgat ctggaacgac aacgagcagg cgctggatga acacattgac 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1954
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1954
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaattttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg cagcggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acacgctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggtttttg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgccca actgtatctg gcgattaagg aagtggttgg taaggcaccg 1560
agcaaagatc gtccgctgat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 1956
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1956
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Ser Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met	195	200		205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215		220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230		235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Ala	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280		285
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295		300
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310		315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345		350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360		365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375		380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390		395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	420	425		430
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440		445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455		460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470		475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505		510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Leu	Ile	Trp	515	520		525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535		540
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550		555
Ser	Ser																		560

<210> 1957
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1957
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tacgggtgca aggcgcgcct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgacgctttg cgaatttggg 480
 agcatcgggtg cgagcgggtga cctgaccccg ctggcgctaca tcaccgggtgc gctgggtggg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
 ttccaccgtt ttattcacca gtgcaaaccg cacgcgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
 ggcccattg cggacggtat tgcagaaatc gcgaagcaaa tcgagggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
 atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
 gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
 accggtaca gcatcatgcc gctgctgacc ttctacggca actcgtgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
 ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagccgc gcacccgcc actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 1958
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1958
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Ala
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 1959

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1959

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cgggtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tacggtgctg	aggcgcgctt	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaaagt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgctggc	aaaaagctgc	cgctggcgga	tgcttctgctg	360
ggatatgctg	tgcgtgcaaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgct	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgctaca	tcaccggtgc	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcaac	gaacctgctg	720
gctgctgagc	tgggtgcaac	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccgct	ttattcacca	gtgcaaaccc	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgct	gggaacgcga	gctaccacgg	tggaacttcc	1080
atgggccaag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccc	1200
gctagcctgg	tgggtaaac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaac	gcatcatgcc	gctgctgacc	ttcctgggca	actcgtgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaaagc	ttgacctgct	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggtgg	taagaagccg	1560
agcaaagatc	gtccgctgat	ctggaacgac	aacgagcagg	cgctggatga	acacattgct	1620
ctgatcgctg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 1960
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1960
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Glu Ala Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Gln Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Lys Gln Ile Glu Val
 325 330 335

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390				395						400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Lys	Pro	Ser	Lys	Asp	Arg	Pro	Leu	Ile	Trp	
		515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1961

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1961

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcggc 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tacggtgcgg aggcgcgcct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```

```

ttccacccgt ttattcacca gtgcaaaccg cacgcgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggccccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca actcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taagaagccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1962
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1962

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Gly	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Glu	Ala	Arg	Leu	Thr
		35				40					45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70				75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100				105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150				155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met
	195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala	Leu Gln Gly Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His	Gln Cys Lys Pro His Ala
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu	Glu Leu Leu Gln Gly Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser	His Asp Tyr Arg Gly Glu
290	295	300
Gln Pro Ile Gln Asp	Arg Tyr Ser Met Arg	Cys Leu Pro Gln Tyr Thr
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile	Ala Lys Gln Ile Glu Val
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu	Ile Asp Val Ala Gly Asn
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly	Gln Tyr Ile Gly Thr Ser
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu	Leu Ala Lys His Leu Asp
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu	Phe Asn Asn Gly Leu Pro
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Pro	Val Asn Met Gly Leu Lys
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met	Pro Leu Leu Thr Phe Tyr
420	425	430
Gly Asn Ser Leu Thr	Asp Arg Phe Pro Thr	His Ala Glu Gln Phe Asn
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser	Ala Asn Leu Thr Arg Gln
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala	Ile Ala Leu Met Phe Gly
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys	Ile Ala Asn His Tyr Asp
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Arg	Gln Leu Tyr Leu Ala Ile
500	505	510
Lys Glu Val Val Gly	Lys Lys Pro Ser Lys	Asp Arg Pro Tyr Ile Trp
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His	Ile Ala Leu Ile Ala Glu
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln	Ala Ile Asn Gln Val Val
545	550	555
Ser Ser		

<210> 1963

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1963

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggtg aagtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggcgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca actcgtgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1964

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1964

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Glu Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
			100					105					110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
		115					120					125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
	130					135					140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145					150					155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170						175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
		195					200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
	210					215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225					230					235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305					310					315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
			500					505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515					520					525				

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1965
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1965

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcggc	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tgttgcgctg	120
tatgggtgca	aggcgctct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcggg	tggtcgtgctg	360
ggatatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gatggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	cacgcgggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcaccggca	actcgtgac	cgatcgcttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgc	gcacccgcc	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1966
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1966

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Gly	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Ala
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Thr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470				475						480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550				555						560		
Ser	Ser																

<210> 1967

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1967

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgct tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtagc aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcaccggca actcgctgac cgatcgcttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgc gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgctgat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1968
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1968
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285

```

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Thr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Leu	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1969

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1969

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcgga gcggtatccg tctggagctg 420

```



```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca actcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag tactatatg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgctgat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac caagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1970
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1970
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```

				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
	275					280						285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290				295						300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420				425							430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Tyr	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475						480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Leu	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1971

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cggatgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tatggtgcca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggatggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggatgcggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgatca tcaccggtgc gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttacatagg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca actcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taagaagccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 1972
<211> 562
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1972

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
```

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
50						55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
130						135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
210						215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
290						295					300						
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
370						375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390						395				400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
450						455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Lys	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1973

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1973

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	aggtggccgc	tggtgcgcgt	120
tacggtgcgg	aggcgcgcct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaagc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gatggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aacaaccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccatttg	cggacggtat	tgcagaaatc	gcgaagcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtccg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcaccggca	acacgctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgc	gcacccgcc	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtacat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 1974
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1974

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Glu	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acacgctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgcgcca actgtatctg gcgattaagg aagtgggttg ttcggcaccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1976
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1976
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```


Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
			325					330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
		340					345						350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
	355						360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505						510		
Lys	Glu	Val	Val	Gly	Ser	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535						540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1977

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1977

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgcgt 120
tacgggtgcga aggcgcgcct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaaact ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc aaaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcgggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcgg tgatgaccgg tattgctggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctgggca acacgctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 1978

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1978

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165				170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210				215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245				250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280					285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355				360						365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405				410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
4															

545
Ser Ser

550

555

560

<210> 1979
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1979
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
ctgggtgctg aggcgagcct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgtaac tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg cacgcgggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aacaaccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca actcgtgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgctg aggatattac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1980
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1980

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ala	Ala	Val	Ala	Arg	Leu	Gly	Ala	Glu	Ala	Ser	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
	195						200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Ala
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440				445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500						505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1981

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1981

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg cagccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcaagcaaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgcatt gttaacatgg gcctgaaggg gctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500

```

<400>	1982														
Met 1	Ile	Ile	Ala	Ser 5	Gln	Thr	Gln	Thr	Phe 10	Thr	Ser	Lys	Ser	Pro	His
Thr	Ala	Ser	Asp 20	Ser	Val	Val	Thr	Val 25	Gly	Asp	Lys	Pro	Leu 30	Thr	Ile
Asn	Glu	Val 35	Ala	Ala	Val	Ala	Arg 40	Tyr	Gly	Ala	Lys	Ala 45	Arg	Leu	Thr
Asp	Lys 50	Glu	Glu	Val	Leu	Gln 55	Arg	Val	Asn	Ala	Ser 60	Cys	Glu	Trp	Val
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn	Asn 100	Leu	Pro	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys
Leu	Pro	Leu 115	Ala	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg 125	Ala	Asn	Ser
His	Leu 130	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu	Leu 140	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His 155	Val	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro 170	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn 190	Gly	Glu
Glu	Met	Thr 195	Ala	Pro	Glu	Ala	Leu 200	Lys	Arg	Leu	Gly	Leu 205	Glu	Pro	Leu
Glu	Leu 210	Gln	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	Tyr	Asp 235	Ala	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala 250	Leu	Gln	Gly	Leu	Asn 255	Gly
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile 275	Trp	Ser	Ala	Gln	Gln	Met 280	Leu	Glu	Leu	Leu 285	Gln	Gly	Ser
Gln	Leu 290	Ile	Arg	Asp	Glu	Leu 295	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Ile	Val	Asn	Met	Gly	Leu Lys
			405					410						415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
			420				425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440						445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Gln
	450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala Ile
		500					505						510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520						525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530					535					540			
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550					555					560
Ser	Ser													

<210> 1983
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1983
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600


```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tggccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatt gttaacatgg gcctgaaggg gctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgcga actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 1984

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1984

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```

<210> 1985
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1985

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtggccgc tgttgccgct 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaagc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccggt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacagccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaagcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcctg gttaacatgg gcctgaaggg gctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgccca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 1986

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1986

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ala Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Leu	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 1988

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
		530					535					540			
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 1989

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1989

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	agggtgtcggc	tggttgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggg	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccgggtg	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgtggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagtctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg caaccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 1990
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1990
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 1992
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 1992
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200		205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215		220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230		235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280		285
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295		300
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310		315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345		350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360		365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375		380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390		395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425		430
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440		445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455		460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470		475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505		510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520		525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535		540
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550		555
Ser	Ser																		

<210> 1993
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1993
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacgggtac caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagtctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagccgc gcaccgccca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 1994
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1994
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				

450		455		460
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly				
465		470		480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp				
	485		490	495
Ala Ser Gln Leu Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile				
	500		505	510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp				
	515		520	525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu				
	530		535	540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val				
545		550		560
Ser Ser				

<210> 1995

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1995

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cgggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgctg	120
tatggtgcca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttgg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgagggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acagtctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttgg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtacat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 1996

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1996

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val
      325     330     335

```

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 1997

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1997

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```



```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gctaatacaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg caaccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgac 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgctgaa ccaagtgggt 1680
agcagt 1686

```

<210> 1998

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1998

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala Leu Gln Gly	Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His Gln Cys Lys	Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu Glu Leu Leu Gln Gly	Ser
275	280	285
Leu Leu Ile Arg Asp	Glu Leu Asp Gly Ser His Asp Tyr Arg Gly	Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr	
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val	
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn	
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser	
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp	
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro	
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Met Val Asn Met Gly Leu Lys	
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Tyr	
420	425	430
Gly Asn Thr Leu Thr	Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn	
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Gln	
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly	
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp	
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Ala Thr Arg Gln Leu Tyr Leu Ala Ile	
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp	
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu	
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln Ala Leu Asn Gln Val Val	
545	550	555
Ser Ser		

<210> 1999

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 1999

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcagaaatc gctaataaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2000

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2000

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
			500					505					510				
Lys	Glu	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp			
		515				520					525						

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2001
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2001

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgctg	120
tatgggtgca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggttggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcggg	tggtcgtgcg	360
ggatatgctg	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggtttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	accgcgtgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaa	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgttttgg	1440
gtgcaaagcg	ttgacctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgc	gcacccgcca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2002
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2002

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys


```

ccgaccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2004
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2004
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
275          280          285

```


Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2005

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2005

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctggggca acagtctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2006
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2006
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```


<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2007
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagagg ggttgccaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc ggggtgcggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgaggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcagaaatc gctaataaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatagg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccgg caaccgcga actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2008
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2008
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35 40 45

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2009

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2009

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cgggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tggttcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taactcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcggaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttggg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccatttg	cggacgggtat	tgcagaaatc	gctaatacaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acactctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcggaac	1380
ctgaccctgc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccgg	caaccgcga	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtacat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	caaagatggc	cgtattgttc	aggcgctgaa	ccaagtgggt	1680
agcagt						1686

<210> 2010
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2010

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgcagaaatc gctaatacaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccgg caaccgccca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgctgaa ccaagtgggt 1680
agcagt
1686

```

<210> 2012
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2012
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Thr Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325					330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485						490					495	
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Leu	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2013

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2013

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgctg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtg tgcagaaatc gctaatacaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg caaccgccca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 2014

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2014

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210				215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345						350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450				455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly

545
Ser Ser

550

555

560

<210> 2015
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2015
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gctaatacaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctgggca acagtctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2016
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2016

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2017

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2017

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggc cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaactg 1500

```

ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtggttgg	taaggcgccg	1560
agcaaagatc	gtccgtacat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgttt	1680
agcagt						1686

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu Lys
			405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
		420				425							430	
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Gln
	450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490					495	
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala Ile
		500				505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530				535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550				555						560
Ser	Ser													

<210> 2019
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2019
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
 tgcgagtggg tggcgaccgc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcgggtggca tggcgaacct gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcggg tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gctaataaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttcctgggca acagtctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg caccgccca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2020
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2020
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Thr Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190

```

<210>	2021
<211>	1686
<212>	DNA
<213>	Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2021

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta ca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acagtctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2022

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2022

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
				100					105					110	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
				115					120					125	
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
				130					135					140	
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
				145					150					155	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
				180					185					190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
				195					200					205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
				210					215					220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
				225					230					235	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
				260					265					270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
				275					280					285	
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
				290					295					300	
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
				305					310					315	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
				340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
				355					360					365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
				370					375					380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
				385					390					395	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
				420					425					430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435					440					445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
				450					455					460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
				465					470					475	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn			

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2024

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Lys	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20				25						30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500						505				510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
		530					535					540			
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2025

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2025

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	agggtgcggc	tggttgcgct	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgaccgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140


```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagtctgac cgatcgtttc 1320
ccgaccacacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2026

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2026

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Thr Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcacccgcc actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 2028

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2028

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Lys Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200		205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215		220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230		235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280		285
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295		300
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310		315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345		350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360		365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375		380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390		395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	420	425		430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440		445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455		460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470		475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505		510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520		525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535		540
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550		555
Ser	Ser																		

<210> 2029
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2029
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgaccc cgacgcttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgctaca tcaccgggtgc gctgggtggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcaccgccca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2030
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2030
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420				425				430				

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 2031

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2031

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	aggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgctg	120
tatggtgcca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacgggtcga	gcggatatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacagtttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggtggg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgagggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgt	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtacat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 2032

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2032

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Lys Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Leu Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val
      325     330     335

```


Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
		420						425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2033

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2033

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta aggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```

```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gctaatacaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagtctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccgg caaccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2034
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2034
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Lys Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala	Leu Gln Gly Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His	Gln Cys Lys Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu	Glu Leu Leu Gln Gly Ser
275	280	285
Leu Leu Ile Arg Asp	Glu Leu Asp Gly Ser	His Asp Tyr Arg Gly Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg	Cys Leu Pro Gln Tyr Thr
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile	Ala Asn Gln Ile Glu Val
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu	Ile Asp Val Ala Gly Asn
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly	Gln Tyr Ile Gly Thr Ser
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu	Leu Ala Lys His Leu Asp
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu	Phe Asn Asn Gly Leu Pro
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Met	Val Asn Met Gly Leu Lys
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met	Pro Leu Leu Thr Phe Tyr
420	425	430
Gly Asn Ser Leu Thr	Asp Arg Phe Pro Thr	His Ala Glu Gln Phe Asn
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser	Ala Asn Leu Thr Arg Gln
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala	Ile Ala Leu Met Phe Gly
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys	Ile Ala Asn His Tyr Asp
485	490	495
Ala Ser Gln Leu Leu	Ser Pro Ala Thr Arg	Gln Leu Tyr Leu Ala Ile
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys	Asp Arg Pro Tyr Ile Trp
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His	Ile Ala Leu Ile Ala Glu
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln	Ala Ile Asn Gln Val Val
545	550	555
Ser Ser		

<210> 2035

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2035

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta aggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acactctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccgc gcaccgcca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 2036

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2036

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Lys Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
				325				330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515					520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2037
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2037
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
 tatgggtgca aggcgctctt gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtt taccactggg 240
 ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgctttg cgaatttggg 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataacct tgatttttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
 ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
 gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaaca gcatcatgcc gctgctgacc ttctacggca acagtctgac cgatcgcttc 1320
 ccgaccacg cgagcagttt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
 ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
 ctgagcccgg caaccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
 agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
 ctgatcgagg aggatattac caaagatggc cgtattgttc aggcgctgaa ccaagtgggt 1680
 agcagt 1686

<210> 2038
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2038

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Leu	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ser																

<210> 2039

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2039

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc ggtaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaac gcatcatgcc gctgctgacc ttctgggca acagtctgac cgatcgtttc 1320

```



```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttgg cagcgcggaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgttttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg caacccgccca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2040
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2040
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
275          280          285

```

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Gly	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2041

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2041

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtggtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gctaataaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccgg caaccgccca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2042
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2042
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```

				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
		420					425						430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2043
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagagg ggttgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcagaaatc ggtaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatagg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaactg 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2044
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2044
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35 40 45

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val		
50						55					60						
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly		
65					70					75					80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu		
				85					90					95			
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys		
		100					105						110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
	115					120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
130						135						140					
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145				150						155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
	195						200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
210						215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280						285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
290						295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Gly	Asn	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
370						375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390						395				400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
450						455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Leu	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2045

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2045

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tggtgcgctg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taactcgagc	180
tgcgagtggg	tggcgaccgc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccgct	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccattg	cggacgggtat	tgcagaaatc	gctaatacaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acagtctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaactg	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcgg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2046
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2046

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Thr	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100					105						110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgcagaaatc gctaatacaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcctgggca acagtctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg caaccgcga actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2048
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2048
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Thr Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
		420						425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515						520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2049

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2049

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta aggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggg aaaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggcg tgatgaccgg tattgcccgg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacgggtg caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtt tgcagaaatc gctaatacaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaac gcatcatgcc gctgctgacc ttctggggca acagtctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcaaac 1380
ctgaccgcgt aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgcg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 2050

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2050

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Lys Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

[illegible]

545
Ser Ser

550

555

560

<210> 2051
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2051
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taactcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgta caaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctgggca acagtctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagccgc gcaccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2052
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2052

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ser	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2053

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2053

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcggt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggc cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gtagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500

```


305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu Lys
			405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
		420				425							430	
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Gln
	450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala Ile
		500				505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530				535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550				555						560
Ser	Ser													

<210> 2055
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2055
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta cggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcggtggca tggcgaacct gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc ggggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccgg caaccgccca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2056
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2056
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2057

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2058

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2058

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
	195					200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2060

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Lys	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20				25						30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500						505				510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
		530					535					540			
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2061

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2061

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	agggtgcggc	tggtgcgctg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taactcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaga	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttgtag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccatttg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtggttg taaggcgccg 1560
agcaaagatc gtccgtacat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

```

<210> 2062
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 2062
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ser Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtag cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acagtctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccgccca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 2064
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2064
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200		205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215		220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230		235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280		285
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295		300
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310		315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345		350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360		365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375		380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390		395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	420	425		430
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440		445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455		460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470		475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505		510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520		525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535		540
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550		555
Ser	Ser																		560

<210> 2065
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2065
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg cagccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcaccgccca actgtatctg gcgattaagg aagtgggtgg tagcactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2066
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2066
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Gln	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Ser Thr Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Gly Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 2067

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2067

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgctg	120
caggggtgca	aggcgcgtct	gacggacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacgggtcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gatggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgagggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaaacac	cgaccgtatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	aaagcattga	aatcttccaa	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcgg	taaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 2068

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2068

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Gln Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Met
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Gln Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val
      325     330     335

```



```

ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggccccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cccccgcca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2070
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2070
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Met
195    200    205
Glu Leu Gln Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala	Leu Gln Gly Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His	Gln Cys Lys Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu	Glu Leu Leu Gln Gly Ser
275	280	285
Gln Leu Ile Arg Asp	Glu Leu Asp Gly Ser	His Asp Tyr Arg Gly Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg	Cys Leu Pro Gln Tyr Thr
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile	Ala Asn Gln Ile Glu Val
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu	Ile Asp Val Ala Gly Asn
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly	Gln Tyr Ile Gly Thr Ser
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu	Leu Ala Lys His Leu Asp
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu	Phe Asn Asn Gly Leu Pro
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Met	Val Asn Met Gly Leu Lys
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met	Pro Leu Leu Thr Phe Tyr
420	425	430
Gly Asn Ser Leu Thr	Asp Arg Phe Pro Thr	His Ala Glu Gln Phe Asn
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser	Ala Asn Leu Thr Arg Gln
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala	Ile Ala Leu Met Phe Gly
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys	Ile Ala Asn His Tyr Asp
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Arg	Gln Leu Tyr Leu Ala Ile
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys	Asp Arg Pro Tyr Ile Trp
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His	Ile Ala Leu Ile Ala Glu
530	535	540
Asp Ile Gly Lys Asp	Gly Arg Ile Val Gln	Ala Ile Asn Gln Val Val
545	550	555
Ser Ser		

<210> 2071

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2071

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
cagggtgcga aggcgcgtct gacggacaaa gcggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggcgcga gcggatatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacac cgaccgtctg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg aaagcattga aatcttccaa caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaagctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgtgg aggatatcac gaaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 2072

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2072

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Gln Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Ala Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Leu	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515					520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Val	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2073
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2073

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgctg	120
tatgggtgca	aggcgcgtct	gacggacaaa	gcggaagtgc	tcagcgtgtg	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggttggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tggtcgtgctg	360
ggatatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgacggtttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgctaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgtggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgctg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaa	cgctgtgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgttttgg	1440
gtgcaaagcg	ttgacctgctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgc	gcacccgcc	actgtatctg	gcgattaagg	aagtgggttg	taaaactccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcg	aggatatcac	gaaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2074
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2074

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Ala	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr		
			420					425					430				
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485				490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515						520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550				555						560		
Ser	Ser																

<210> 2075

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2075

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggcgcgtct gacggacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtagc aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgc gcacccgcca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac gaaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2076
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2076
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Met
195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
275          280          285

```

Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290					295						300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370						375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
450						455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2077

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2077

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggcgcgtct gacggacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg cagccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgctgt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2078
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2078
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```


<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2079

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcca aggcgcgtct gacggacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc ggttgccaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg cagccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttacatagg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgc gcaccgccca actgtatctg gcgattaagg aagtgggttg taaagctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac gaaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2080
<211> 562
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2080

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
```

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Gln	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr	
			420					425					430			
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
450						455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2081

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2081

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tggttcgcgt	120
caggggtgca	aggcgcgtct	gacggacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gatggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccatttg	cggacgggtat	tgcagaaatc	gcgaatcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgtatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttctacggca	acagcctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgc	gcacccgcc	actgtatctg	gcgattaagg	aagtgggttg	tagcactccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcgg	taaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2082
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2082

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Gln	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtctg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgcgcca actgtatctg gcgattaagg aagtgggttg tagcgctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2084

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2084

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Gln Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325				330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Leu	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
		420					425						430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500				505						510		
Lys	Glu	Val	Val	Gly	Ser	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Gly	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 2085

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2085

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgta caaccgggtg gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcccgg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaac gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgcgt aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcaccgccca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 2086

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2086

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

[illegible]

545
Ser Ser

550

555

560

<210> 2087
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2087
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gatggaactg cagccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtctg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccaa caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaaactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatattcac gaaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2088
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2088

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met
		195					200					205			
Glu	Leu	Gln	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Leu	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		

Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2089

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2089

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
cagggtgcgc ctgctgctct gacggacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctg aaagcattga aatcttccaa caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500

```

ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtggttgg	taaagctccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattg	1620
ctgatcg	aggatatcg	taaagatggc	cgtattgttc	aggcgatcaa	ccaagtgtt	1680
agcagt						1686

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu Lys
			405					410						415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Tyr
			420				425						430	
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440						445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Gln
	450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala Ile
		500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520						525		
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530					535					540			
Asp	Ile	Gly	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550					555					560
Ser	Ser													

<210> 2091
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2091
 atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
 tatggtgctg gtgcgctct gacggacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
 ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc caaagctgc cgctggcggc tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcgtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaacgcctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgcgtc aaagcattga aatcttccaa caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgcga actgtatctg gcgattaagg aagtggttgg tagcgctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 2092
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2092
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
           20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Arg Ala Arg Leu Thr
           35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
           50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
           85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
           100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
           115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
           130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
           165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
           180          185          190

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2093

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
caggggtgca aggcgcgtct gacggacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gatggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgtctg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttccaa caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtggttgg taaagctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgtgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2094

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2094

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Gln Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Met
	195					200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Leu	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2096

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Gln	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Leu	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Ser	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Val	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2097

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2097

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	ctgtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tggtgcgctg	120
tatggtgcga	aggcgcgtct	gacggacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgtaga	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgagca	gaacctgctg	720
gcgctgagcc	tgggtgagca	tgctgctggc	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccg	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttgtag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagccagctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccattg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccag	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgacccacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccaa caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtgggttg taaaactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac gaaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2098

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2098

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaattttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgtctg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcacccgcc actgtatctg gcgattaagg aagtggttgg taaagctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac gaaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 2100
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2100
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

[illegible]

<210> 2101
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2101
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta ctgtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
cagggtgcga aggcgcgtct gacggacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggcgtgaccc cgacgcttg cgaatttggg 480
agcatcggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgtgg aggatcac gaaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2102
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2102
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Gln	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420				425				430				

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Val Glu					
	530		535		540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 2103

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2103

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgt taccactggc 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc ggggtgcggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgag ggcgtgacct cgacgctttg cgaatttggc 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgatca tcaccggtgc gctgggtggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgga tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagca tgggtgcccc tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccgggttc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg tagacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cgagcagatt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcacccgcca actgtatctg gcgatccgcg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680

```

<210> 2104
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2104
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Met Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Leu Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Val Asp Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val
 325 330 335


```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acactattac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcggtccgcg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgac 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2106
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2106
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala	Leu Gln Gly Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His	Gln Cys Lys Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu	Glu Leu Leu Gln Gly Ser
275	280	285
Leu Leu Ile Arg Asp	Glu Leu Asp Gly Ser	His Asp Tyr Arg Gly Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg	Cys Leu Pro Gln Tyr Thr
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile	Ala Asn Gln Ile Glu Val
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu	Ile Asp Val Ala Gly Asn
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly	Gln Tyr Ile Gly Thr Ser
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu	Leu Ala Lys His Leu Asp
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu	Phe Asn Asn Gly Leu Pro
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Met	Val Asn Met Gly Leu Lys
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met	Pro Leu Leu Thr Phe Leu
420	425	430
Gly Asn Thr Ile Thr	Asp Arg Phe Pro Thr	His Ala Glu Gln Phe Asn
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser	Ala Asn Leu Thr Arg Gln
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala	Ile Ala Leu Met Phe Gly
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys	Ile Ala Asn His Tyr Asp
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Arg	Gln Leu Tyr Leu Ala Val
500	505	510
Arg Glu Val Val Gly	Lys Ala Pro Ser Lys	Asp Arg Pro Tyr Ile Trp
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His	Ile Ala Leu Ile Ala Glu
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln	Ala Ile Asn Gln Val Val
545	550	555
Ser Ser		

<210> 2107

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2107

```
atgatcattg cgagccagac ccaaaccttc accagccaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgag ggctgacct cgacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcccc tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtagc aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcggtcaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2108

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2108

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Gln Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```

Leu 100	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
Leu 110	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
His 115	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
Glu 120	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
Ser 125	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
Ala 130	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu 135	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
Met 140	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
Met 145	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
Ala 150	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
Thr 155	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
Gly 160	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Leu 165	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
Asp 170	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
Gly 175	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
Glu 180	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
Ala 185	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
Met 190	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
Val 195	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
Ala 200	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
Gly 205	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
Gly 210	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
Gln 215	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
Ser 220	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
Val 225	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
Ala 230	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
Lys 235	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2109
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2109
 atgatcattg cgagccagac ccaaaccttc accagcagta gtccgcacac cgccagcgac 60
 agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
 tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctggttggg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgccc tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
 ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
 gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
 ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgc gcacccgcca actgtatctg gcggtcaagg aagtggttgg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 2110
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2110

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Ser	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
			420					425					430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ser																

<210> 2111

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2111

```

atgatcattg cgagccagac ccaaaccctt accagcagta gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtagga tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgtggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgacctg cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgacctg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcccc tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaac gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgttttgt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgc gcacccgcca actgtatctg gcgatcaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2112
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2112
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Ser Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
275          280          285

```

Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425						430	
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2113

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2113

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtgcca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2114
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2114
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```


<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2115
atgatcattg cgagccagac cgataccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagagg ggttgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttgg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gctgtagacc tgggtgcgca tgcgtggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2116
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2116
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35 40 45

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355						360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
			420					425					430			
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2117

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2117

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tggtgcgcgt	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgccaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccgggtg	gctgggtggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttgtag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccatttg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtaga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaca	gcatcatgcc	ggtgctgacc	ttcctgggca	acactctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcgg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2118
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2118

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgcgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2120
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2120
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Gly Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265					270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280					285				
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310					315						320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
			325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370				375				380							
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385				390					395						400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
		420				425						430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435				440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450				455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465				470					475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530				535						540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545				550					555						560	
Ser	Ser															

<210> 2121

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2121

atgatcattg atagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaaca tcaccgggtg gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtgaaca gcatcatgcc gctgctgacc ttctggggca acactctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caaccaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgcgcca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 2122

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2122

```

Met Ile Ile Asp Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115						120				125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470											

545
Ser Ser

550

555

560

<210> 2123
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2123
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2124
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2124

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		

Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
		500					505						510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 2125

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2125

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacca ggccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggctgacctc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgctaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggtttttg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500

```

ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtggttgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattg	1620
ctgatcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgtt	1680
agcagt						1686

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu Lys
			405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Leu
		420				425							430	
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Gln
	450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala Ile
		500				505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530				535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550				555						560
Ser	Ser													

<210> 2127
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2127
 atgatcattg cgagccagac ccaaacccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta cggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
 tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcgggtggca tggcgaacct gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg gttcaggggc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgcgtc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgccca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2128
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2128
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2129

```
atgatcattg cgagccagac ccaaaccttc gatagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2130

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2130

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Asp Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2132

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Arg	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2133

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2133

atgatcattg	cgagccagac	ccaaaccttc	gcgagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	agggtgcggc	tggtgcgcg	120
tatggtgcga	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtg	360
ggatatgctg	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgtaga	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttgtag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	cggacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cgcacccgcca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2134
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2134
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Ala Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgacccc cgcacgtttg cgaattttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctggggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcacccgcc actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 2136
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2136
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Ser Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200		205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215		220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230		235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280		285
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295		300
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310		315
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345		350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360		365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375		380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390		395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	420	425		430
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440		445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455		460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470		475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	500	505		510
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520		525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535		540
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550		555
Ser	Ser																		

<210> 2137
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2137
atgatcattg cgagccagac ccgtaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggt tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gctgtagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccc caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcaccgccca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2138
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2138
Met Ile Ile Ala Ser Gln Thr Arg Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420				425				430				

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 2139

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2139

atgatcattg	cgagccagac	ccaaaccttc	aagagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cgggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgctg	120
tatggtgcca	aggcgcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgccaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgctggc	caaaagctgc	cgctggcgga	tgcttctgctg	360
ggatatgctg	tgcgtgcaaa	cagccacctg	cacgggtgca	gcggatatccg	tctggagctg	420
attcagcgta	tcgaaacctt	cctgaacgag	ggcgtgaccc	cgacagcttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcgtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaaggaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcaaa	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccc	caccggggtc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgc	gcagtatacc	960
ggcccgaattg	cggacgggtat	tgcagaaatc	gcgaatcaaa	tcgagggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgctg	gggaacgcga	gctaccacgg	tggaacttcc	1080
atgggccaagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccc	1200
gctagcctgg	tgggtaaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggttaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acactctgac	cgatcgtttc	1320
ccgaccacag	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaaagc	ttgacctgca	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccg	gcacccgcca	actgtatctg	gcgattaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgca	1620
ctgatcgcgg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680

<210> 2140

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2140

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Lys Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Leu Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320
Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val
      325     330     335

```

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
		420						425					430			
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2141

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2141

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgctcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```

```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gcgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgac 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2142
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2142

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75				80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100					105						110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala Leu Gln Gly	Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His Gln Cys Lys	Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu Glu Leu Leu Gln Gly	Ser
275	280	285
Leu Leu Ile Arg Asp	Glu Leu Asp Gly Ser His Asp Tyr Arg Gly	Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr	
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val	
325	330	335
Glu Ile Asn Ser Ala	Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn	
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser	
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp	
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro	
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Met Val Asn Met Gly Leu Lys	
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met Pro Leu Leu Thr Phe Leu	
420	425	430
Gly Asn Thr Leu Thr	Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn	
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Gln	
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly	
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp	
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Ile	
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp	
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu	
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val	
545	550	555
Ser Ser		

<210> 2143

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2143

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgcccatgac 60
agcgtggtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgacct cgacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatga tcaccgggtg gctgggtggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctgt ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggc cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtagc aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgcgcg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatagg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2144

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2144

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala His Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
			420					425					430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
			500					505					510				
Lys	Glu	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp			
		515				520					525						

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2145
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2145
 atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
 tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgtg tcgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttggg 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
 atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
 ggcccgatta gggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
 gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
 ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgc gcacccgcca actgtatctg gcgattaagg aagtgggtgg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 2146
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2146

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Ala	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Arg	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
			420					425					430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550					555					560		
Ser	Ser																

<210> 2147

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2147

```

atgatcattg cgagccagac cgggaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg tcgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatt gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgttttgt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgc gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2148
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2148
Met Ile Ile Ala Ser Gln Thr Gly Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225         230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245         250         255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260         265         270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275         280         285

```

Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425						430	
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2149

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2149

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcgga gcggtatccg tctggagctg 420

```

```

attcagcgtc ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcgat gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctggggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2150
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2150
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Leu
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```

				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
		420					425						430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470						475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2151
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggcgcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaaact gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta tcgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggat ggcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatagg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgc gcaccgccca actgtatctg gcgattaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2152
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2152
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Ala Arg Leu Thr
35 40 45

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Met	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355						360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
			420					425					430			
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Ile
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2153

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2153

atgatcattg	ctagccagac	cgataccttc	gacagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tggttcgcgt	120
tatggtgcga	aggttcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttggag	cgcgacgcaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	ccgacgggtat	tgcagaaatc	gcgaatcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acactctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	ccaccgccca	actgtatctg	gcggtcaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2154
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2154

Met	Ile	Ile	Ala	Ser	Gln	Thr	Asp	Thr	Phe	Asp	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
		100					105						110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg tgcacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccaccgccca actgtatctg gcggtaaggg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2156
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2156
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1      5      10      15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
		420						425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2157

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2157

atgatcattg atagccagac ccagaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggcg tgatgaccgg tattgcccgc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcccgc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg ccgacgggtat tgcagaaatc gcaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttctggggca acactctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caaccaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccgcgt aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgcg gtaccgccca actgtatctg gcggtcaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 2158

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2158

```

Met Ile Ile Asp Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

	115						120						125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile			
	130					135					140							
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly			
145					150					155					160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly			
					165					170					175			
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val			
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu			
225					230					235					240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly			
					245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu			
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr			
305					310					315					320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val			
					325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro			
385					390					395					400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu			
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly			
465					470					475					480			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp			
	</																	

545
Ser Ser

550

555

560

<210> 2159
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2159
atgatcattg atagccagac ccagaccttc actagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc ggttgcaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctgc tgcgtgcaaa cagccacctg cacgggtgca gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaaa tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcaaa tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccc caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgctggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg ccgacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtgaaca gcatcatgcc ggtgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gtacccgcca actgtatctg gcgggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgagg aggatattac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2160
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2160

Met	Ile	Ile	Asp	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Val	Leu	Thr	Phe	Leu
			420					425					430		

Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val	
		500						505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2161

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2161

```

atgatcattg atagccagac ccgtaccttc gacagccgta gtccgcacac cgccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggc cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg ccgacggtat tgcagaaatc gcgaatcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gtagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500

```

```

ctgagccccg ccacccgcca actgtatctg gcggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgaggatatacac caaagatggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

<210> 2162
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2162

Met	Ile	Ile	Asp	Ser	Gln	Thr	Arg	Thr	Phe	Asp	Ser	Arg	Ser	Pro	His	1	5	10	15
Thr	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile	20	25	30	
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr	35	40	45	
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	50	55	60	
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	65	70	75	80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	85	90	95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys	100	105	110	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	115	120	125	
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	130	135	140	
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170	175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr				

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu Lys
			405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Leu
		420				425							430	
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Gln
	450				455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala Val
		500				505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530				535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550				555						560
Ser	Ser													

<210> 2163
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2163
 atgatcattg atagccagac ccagaccttc actagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
 tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcgggtggca tggcgaacct gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
 attcagcgta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtg gctgggttggt 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cgtaccgcca actgtatctg gcggtcaagg aagtggttgg taaggctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2164
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2164
Met Ile Ile Asp Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
           20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
           35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
           50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
           85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
           100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
           115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
           130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
           165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
           180          185          190

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2165

```
atgatcattg cgagccagac ccagaccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatagg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gtaccgcca actgtatctg gcggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgctg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2166

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2166

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Asp Ser Lys Ser Pro His
1           5           10          15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```


65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
	195					200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2168

Met	Ile	Ile	Asp	Ser	Gln	Thr	Asp	Thr	Phe	Gly	Ser	Lys	Ser	Pro	His
1				5					10					15	
Pro	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Val	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490						495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500						505				510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
		530					535					540			
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2169

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2169

atgatcattg	atagccagac	cgataccttc	actagcaaaa	gtccgcacac	cgccagcgac	60
agcaccgtta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgcgt	120
tatggtgcga	aggttcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	aaaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccggtgc	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgctgtggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgtag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	ccgacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgctg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcgggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggtt 1680
agcagt 1686

```

```

<210> 2170
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 2170
Met Ile Ile Asp Ser Gln Thr Asp Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg cagggctgca gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaattttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
tcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg ccgacggtat tgcagaaatc gcgaatcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggtttttg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cgtaccgcca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgc taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 2172
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2172
Met Ile Ile Asp Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Gln Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

[illegible]

<210> 2173
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2173
atgatcattg ctagccagac ccagaccttc ggcagccgta gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgtg ttgaaacctt cctgaacgcg ggcgtgaccc cgacgcttg cgaatttggg 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg ccgacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg ccacccgcca actgtatctg gcggtcaagg aagtgggtgg taaggctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2174
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2174
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Gly Ser Arg Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420				425				430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
			435				440				445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Arg Gln Leu Tyr Leu Ala Val					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 2175

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2175

```

atgatcattg ctagccagac cgataccttc gacagccgta gtccgcacac tgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgctggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgca gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgag ggcgtgacct cgacgtttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgta taccgggtgc gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg tcgacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcggaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gtaccgccca actgtatctg gcggtcaagg aagtgggtgg taaggctccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatattac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680

```

<210> 2176

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2176

```

Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Arg Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Leu Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
          290          295          300
Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305          310          315          320
Gly Pro Ile Val Asp Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val
          325          330          335

```

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
		420						425					430			
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2177

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2177

```

atgatcattg atagccagac ccgtaccttc gacagcaaaa gtccgcacac cgccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```

```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggccccgattg ccgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaa atcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cccccgcca actgtatctg gcggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 2178

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2178

```

Met Ile Ile Asp Ser Gln Thr Arg Thr Phe Asp Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala	Leu Gln Gly Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His	Gln Cys Lys Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu	Glu Leu Leu Gln Gly Ser
275	280	285
Leu Leu Ile Arg Asp	Glu Leu Asp Gly Ser	His Asp Tyr Arg Gly Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg	Cys Leu Pro Gln Tyr Thr
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile	Ala Asn Gln Ile Glu Val
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu	Ile Asp Val Ala Gly Asn
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly	Gln Tyr Ile Gly Thr Ser
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu	Leu Ala Lys His Leu Asp
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu	Phe Asn Asn Gly Leu Pro
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Met	Val Asn Met Gly Leu Lys
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met	Pro Leu Leu Thr Phe Leu
420	425	430
Gly Asn Thr Leu Thr	Asp Arg Phe Pro Thr	His Ala Glu Gln Phe Asn
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser	Ala Asn Leu Thr Arg Gln
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala	Ile Ala Leu Met Phe Gly
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys	Ile Ala Asn His Tyr Asp
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Arg	Gln Leu Tyr Leu Ala Val
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys	Asp Arg Pro Tyr Ile Trp
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His	Ile Ala Leu Ile Ala Glu
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln	Ala Ile Asn Gln Val Val
545	550	555
Ser Ser		

<210> 2179

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2179

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggatatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgag ggctgacctc cgacgcttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgatca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgcggcg aactgcgttt atgatgtgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacgggtg caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgaggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacgggat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctggggca acactctgac cgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcggtcaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2180

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2180

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```


Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Val	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
			420					425					430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515					520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2181
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2181

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgctg	120
tatgggtgca	aggttcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tgttcgtgctg	360
ggatatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgcg	ggcgtgacct	cgacggtttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataccgt	tgatttttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tatggcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcaggggc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccgggttc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cagacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaa	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acactctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caacaaaaac	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgttttgg	1440
gtgcaaagcg	ttgacctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgc	gcacccgcca	actgtatctg	gcggtcaagg	aagtgggttg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattg	1620
ctgatcgcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2182
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2182

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Met	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
			420					425					430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470				475						480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val		
		500						505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520					525						
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530					535					540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550				555						560		
Ser	Ser																

<210> 2183

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2183

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcagac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacgggtcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaac gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgc gcacccgcca actgtatctg gcggtcaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2184
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2184
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro Gln
1          5          10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225         230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245         250         255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260         265         270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
275         280         285

```

Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2185

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2185

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggttcgtgcg 360
ggatatgtgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctggggca acactctggg ggatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2186
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2186
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```


<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2187
atgatcattg cgagccagac ccaaaccggg accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cggatgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg ttgaaacctt cctgaacgcg ggcgtgacct cgacgtttg cgaatttggg 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatagg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2188
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2188
Met Ile Ile Ala Ser Gln Thr Gln Thr Gly Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35 40 45

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355					360						365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
			420					425					430			
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2189

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2189

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cgggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tggttcgcgt	120
tatggtgcga	aggttcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggg	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtgc	gctgggttggg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccggggtc	aaatttggag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgcacgcc	gcagtatacc	960
ggcccatttg	cagacgggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattgggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtgcaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggctctgccg	1200
gctagcctgg	tgggtaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acactctgac	cgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcggaac	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccg	gcacccgcc	actgtatctg	gcggtcaagg	aagtgggtgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2190
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2190

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120						125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Thr	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgcgcca actgtatctg gcggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2192
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2192
Met Thr Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
	290					295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310					315						320	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
			325					330						335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340					345						350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
	355						360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
	370					375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
			405						410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
		420						425					430			
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435					440						445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val	
		500						505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515						520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550					555					560	
Ser	Ser															

<210> 2193

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2193

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60

```

agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagagg ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaaagt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggcg tgatgaccgg tatggcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tggggggccca tgcgctggcg ctgcaggggc tgaacgggtac caaccatagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctggggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgcgcca actgtatctg gcggtcaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2194

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2194

```

Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```


[illegible]

545
Ser Ser

550

555

560

<210> 2195
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2195
atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcgggtg cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagaaccgaa ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgct gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcgttatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc aggggttttg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgct taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcgggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2196
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2196

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Glu	Pro	Asn	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Val	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		

Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val	
		500						505					510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2197

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2197

```

atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaac tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtg caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgcgcaaat cgcgctgctg accatgccgg agtttaacaa cggtctgccg 1200
gtagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctg aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500

```

ctgagcccg	gcacccgcca	actgtatctg	gcggtcaagg	aagtggttgg	taaggcgccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattg	1620
ctgatcg	aggatatcac	caaagatggc	cgtattgttc	aggcgatcaa	ccaagtgtt	1680
agcagt						1686

```
<210> 2198
<211> 562
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2198															
Met 1	Ile	Ile	Ala	Ser 5	Gln	Thr	Gln	Thr	Phe 10	Thr	Ser	Lys	Ser	Pro	His
Thr	Ala	Ser	Asp 20	Ser	Val	Val	Thr	Val 25	Gly	Asp	Lys	Pro	Leu 30	Thr	Ile
Asn	Glu	Val	Ser 35	Ala	Val	Ala	Arg 40	Tyr	Gly	Ala	Lys	Val 45	Arg	Leu	Thr
Asp	Lys	Glu	Glu	Val	Leu	Gln 55	Arg	Val	Asn	Ala	Ser 60	Cys	Glu	Trp	Val
Ala 65	Gln	Ala	Val	Ala	Lys 70	Gly	Glu	Pro	Ile	Tyr 75	Gly	Val	Thr	Thr	Gly 80
Phe	Gly	Gly	Met	Ala 85	Asn	Val	Val	Ile	Thr 90	Pro	Asp	Gln	Ala	Lys 95	Glu
Leu	Gln	Asn	Asn 100	Leu	Pro	Arg	Tyr	His 105	Lys	Ala	Gly	Ala	Gly 110	Gln	Lys
Leu	Pro	Leu	Ala 115	Asp	Val	Arg	Ala 120	Gly	Met	Leu	Leu	Arg 125	Ala	Asn	Ser
His	Leu	His	Gly	Ala	Ser	Gly 135	Ile	Arg	Leu	Glu	Leu 140	Ile	Gln	Arg	Ile
Glu 145	Thr	Phe	Leu	Asn	Ala 150	Gly	Val	Thr	Pro	His	Val 155	Cys	Glu	Phe	Gly 160
Ser	Ile	Gly	Ala	Ser 165	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly 175
Ala	Leu	Val	Gly 180	Leu	Asn	Asp	Ser	Tyr 185	Thr	Val	Asp	Phe	Asn	Gly	Glu
Glu	Met	Thr	Ala 195	Pro	Glu	Ala	Leu 200	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
Glu	Leu	Leu	Pro	Lys	Glu	Gly 215	Leu	Ala	Met	Met	Asn 220	Gly	Thr	Ala	Val
Met 225	Thr	Gly	Ile	Ala	Ala 230	Asn	Cys	Val	Tyr	Asp	Ala 235	Gln	Asn	Leu	Leu 240
Ala	Leu	Ser	Leu	Gly 245	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly 255
Thr	Asn	Gln	Ser 260	Phe	His	Pro	Phe	Ile 265	His	Gln	Cys	Lys	Pro	His	Pro
Gly	Gln	Ile	Trp 275	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp 300	Tyr	Arg	Gly	Glu
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr

305					310					315				320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu Val
				325					330					335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly Asn
			340					345					350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr Ser
		355					360					365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu Asp
	370				375						380			
Ala	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu Pro
385				390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu Lys
			405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe Leu
			420					425					430	
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe Asn
	435					440						445		
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg Gln
	450					455					460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe Gly
465				470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr Asp
			485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala Val
		500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile Trp
	515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala Glu
	530					535					540			
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val Val
545				550					555					560
Ser	Ser													

<210> 2199

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2199

```

atgatcattg cgagccagca gcaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacct gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggc tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgccca actgtatctg gcggtcaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 2200
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2200
Met Ile Ile Ala Ser Gln Gln Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2201

```
atgggggattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcggtcaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2202

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2202

```
Met Gly Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2204

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Glu	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2205

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2205

atgatcattg	cgagccagac	ccaaaccttc	accagcaaaa	gtccgcacac	cgccagcgac	60
agcgtgggta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tggtgcgcg	120
tatggtgcga	aggttcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgagggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactgg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tggtcgtgcg	360
ggatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccgggtg	gctgggttg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgca	tgctgctggc	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccggt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	cagacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtgcaa at cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacag cggagcagtt caacaaaaac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gttgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg cgcacccgcca actgtatctg gcgggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgac 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

```

<210> 2206
<211> 562
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

```

<400> 2206
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1      5      10      15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtag cctgaccccg ctggcgtaga tcaccgggtgc gctggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgaattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgccca actgtatctg gcggtcaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 2208
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2208
Met Ile Ile Ala Ser Gly Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```


Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145		150		155		160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		165		170		175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		180		185		190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		195		200		205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		210		215		220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		225		230		235	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		245		250		255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		260		265		270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		275		280		285	
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		290		295		300	
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		305		310		315	
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		325		330		335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		340		345		350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		355		360		365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		370		375		380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		385		390		395	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		405		410		415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		420		425		430	
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		435		440		445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		450		455		460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		465		470		475	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		485		490		495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val		500		505		510	
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		515		520		525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		530		535		540	
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		545		550		555	
Ser	Ser																				560	

<210> 2209
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2209
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgat taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgatga tcaccgggtg gctgggtggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccc caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cgagcagatt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagccgc gcacccgcca actgtatctg gcggtcaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcggcg aggatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2210
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2210
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
1 5 10 15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Ile	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420				425				430				

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Val					
	500		505		510
Lys Glu Val Val Gly Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 2211

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2211

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgtttcgcgt 120
tatggtgcca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga tttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgctggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgag ggcgtgacct cgacgctttg cgaatttggc 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgctaca tcaccgggtg gctgggtggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg cagacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg caccgccca actgtatctg gcggtcaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680

```

<210> 2212
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2212
 Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro His
 1 5 10 15
 Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
 20 25 30
 Asn Glu Val Ser Ala Val Ser Arg Tyr Gly Ala Lys Val Arg Leu Thr
 35 40 45
 Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
 50 55 60
 Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
 65 70 75 80
 Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
 85 90 95
 Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
 100 105 110
 Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
 115 120 125
 His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
 130 135 140
 Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
 145 150 155 160
 Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
 165 170 175
 Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
 180 185 190
 Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
 195 200 205
 Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
 210 215 220
 Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
 225 230 235 240
 Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
 245 250 255
 Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
 260 265 270
 Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
 275 280 285
 Leu Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
 290 295 300
 Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
 305 310 315 320
 Gly Pro Ile Ala Asp Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val
 325 330 335

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
		420						425					430			
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2213

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2213

```

atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgcacac cgccagcgac 60
agcgtgggta cggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggc 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaca tcaccgggtg gctgggtggc 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggatccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```

```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcgttatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgc gcacccgcca actgtatctg gcggtcaagg aagtgggttg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgac 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2214
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2214

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35				40						45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75				80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100					105						110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165						170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
		180						185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala Leu Gln Gly	Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His Gln Cys Lys	Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu Glu Leu Leu Gln Gly	Ser
275	280	285
Leu Leu Ile Arg Asp	Glu Leu Asp Gly Ser His Asp Tyr Arg Gly	Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr	
305	310	315
Gly Pro Ile Ala Asp	Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val	
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu Ile Asp Val Ala Gly Asn	
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly Gln Tyr Ile Gly Thr Ser	
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu Leu Ala Lys His Leu Asp	
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu Phe Asn Asn Gly Leu Pro	
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Met Val Asn Met Gly Leu Lys	
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Val Met Pro Leu Leu Thr Phe Leu	
420	425	430
Gly Asn Thr Leu Thr	Asp Arg Phe Pro Thr His Ala Glu Gln Phe Asn	
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser Ala Asn Leu Thr Arg Gln	
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly	
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp	
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Arg Thr Arg Gln Leu Tyr Leu Ala Val	
500	505	510
Lys Glu Val Val Gly	Lys Ala Pro Ser Lys Asp Arg Pro Tyr Ile Trp	
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu	
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val	
545	550	555
Ser Ser		

<210> 2215

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2215

```
atgatcattg cgagccagac ccaaaccttc accagcaaaa gtccgacgac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggc 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgag ggctgacctc cgacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacctcg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg gcacccgcca actgtatctg gcggtcaagg aagtgggtgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 2216

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2216

```
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Ser Pro Thr
1           5           10          15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
			420					425					430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515					520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2217
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2217
 atgatcattg cgagccagac ccaaaccctt accagcaaaa gtccgcacac cgccagcgac 60
 agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
 tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
 attcagcgta ttgaaacctt cctgaacgcg ggctgaccc cgacggttg cgaatttggg 480
 agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctggttggg 540
 ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
 aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
 ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
 gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
 ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
 atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
 taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
 ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
 gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
 atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
 aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctgccc 1200
 gtagcctgg tgggtaacac cgaccgatg gttacatgg gcctgaaggg tctgcagatt 1260
 accggtaaca gcatcatgcc gctgctgacc ttctggggca acactctgac cgatcgtttc 1320
 ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
 ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
 gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
 ctgagcccgc gctctcgcca actgtatctg gcggtcaagg aagtgggtgg taaggcgccg 1560
 agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
 ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
 agcagt 1686

<210> 2218
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2218

Met	Ile	Ile	Ala	Ser	Gln	Thr	Gln	Thr	Phe	Thr	Ser	Lys	Ser	Pro	His
1				5					10					15	
Thr	Ala	Ser	Asp	Ser	Val	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys

				405					410					415					
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu				
			420					425					430						
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn				
		435					440					445							
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln				
	450					455					460								
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly				
465					470				475						480				
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp				
				485				490						495					
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Ser	Arg	Gln	Leu	Tyr	Leu	Ala	Val				
		500						505					510						
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp				
	515					520						525							
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu				
	530					535					540								
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val				
545					550				555						560				
Ser	Ser																		

<210> 2219

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2219

```

atgatcattg cgagccagac ccaaaccctt accagcaaag ggccgcacac cgccagcgac 60
agcgtgggta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgtggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgtg ttgaaacctt cctgaacgcg ggctgacctc cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg cagacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaac gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgttttgt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgc gcacccgcca actgtatctg gcggtcaagg aagtggttgg taaggcgccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac caaagatggc cgtattgttc aggcgatcaa ccaagtggtt 1680
agcagt
1686

```

<210> 2220
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2220
Met Ile Ile Ala Ser Gln Thr Gln Thr Phe Thr Ser Lys Gly Pro His
1           5           10           15
Thr Ala Ser Asp Ser Val Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285

```

Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425						430	
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Arg	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Ala	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2221

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2221

```

atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tacggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc aaaaagctgc cgctggcgga tggttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420

```

```

attcagcgta ttgaaacctt cctgaacgca ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttcag caatatattg cgatcgcgct gctgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2222
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2222
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10           15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```


				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
		420					425						430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Leu	Phe	Gly		
465				470						475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ser																

<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2223

```
atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cggatgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcggatggc tggcgaaagt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgca ggcgtgacct cgcacgtttg cgaatttggg 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgagg tgatgaccgg tattgaggcg aactgcgttt atgatgcgca gaacctgctg 720
tcgctgagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacgggtg caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgcccgaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gctgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcggtcaagg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgagg aggatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2224
<211> 562
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2224

```
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10          15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
```

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ser	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Ala	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
			420					425					430			
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Leu	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2225

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2225

```

atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcaaca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttcgcgct 120
tacggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgat taacgcgagc 180
tgcgagtggg tggcgcgaggc ggttgcggaag ggtgaaccga ttacggcgt taccactggc 240
ttcgggtggc tggcgaaact gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgca ggcgtgacct cgcacgtttg cgaatttggc 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctgggtggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgcc 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac tgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccaccgccca actgtatctg gcggtcaagg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2226
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2226

Met	Ile	Ile	Ala	Ser	Gln	Thr	Asp	Thr	Phe	Asp	Ser	Lys	Ser	Pro	Gln
1				5					10					15	
Gln	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Ile	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg tgcacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcctgggca acactctgac tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccaccgccca actgtatctg gcggtaaggg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2228
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2228
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1      5      10      15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Ile Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240

```

Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325					330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
		420						425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2229

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2229

atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcacca ggccagcgac 60


```

agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tacgggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagggc ggttgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggatatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgca ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctgggttggt 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgcgt 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
gggtaccgcgg tgatgaccgg tattgcccgg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacgggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctggggca acactctggg tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccaccgccca actgtatctg gcggcaagg aagtgggtgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 2230

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2230

```

Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10           15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210				215						220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280					285				
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290				295						300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435				440						445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450				455						460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly

545
Ser Ser

550

555

560

<210> 2231
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2231
atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcaaca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tacggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtg ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtg cctgaccccg ctggcgtaga tcaccgggtg gctggttggg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgtag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgccc aaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttcttgggca acactctgac tgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gctgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccaccgccca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2232
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2232

Met	Ile	Ile	Ala	Ser	Gln	Thr	Asp	Thr	Phe	Asp	Ser	Lys	Ser	Pro	Gln
1				5					10					15	
Gln	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Ala	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		

Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
	435						440				445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Leu	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
				485				490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
	515					520					525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530				535						540					
Asp	Ile	Gly	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2233
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2233

atgatcattg	ctagccagac	cgataccttc	gacagcaaaa	gtccgcacca	ggccagcgac	60
agcaccgtta	cggtgggtga	taagccgctg	acgatcaatg	agggtgtcggc	tgttgcgctg	120
tatggtgcga	aggttcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tgttcgtgctg	360
ggatatgctgc	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgcg	ggcgtgacct	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgctaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataaccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
tcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	tcgacggtat	tgcagaaatc	gcgaatcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	accgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgcccaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gtagcctgg	tgggtaaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acactctgac	tgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccgctc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gctgtttggg	1440
gtgcaaagcg	ttgacctgctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500

ctgagcccg	ccacccgcca	actgtatctg	gcggtcaagg	aagtggttgg	taagactccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcg	aggatatcgg	taaagatggc	cgtattgttc	aggcgatcaa	ccaagtggtt	1680
agcagt						1686

 $\langle 220 \rangle$

<400> 2234

305					310					315				320	
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Ala	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
		420					425						430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Leu	Phe	Gly
465				470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490					495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
		500				505					510				
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535					540					
Asp	Ile	Gly	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550				555						560	
Ser	Ser														

<210> 2235
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2235
 atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcaaca ggccagcgac 60
 agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
 tacggtgcca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacct gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta ttgaaacctt cctgaacgca ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600

```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacgggat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgccc aaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcctgggca acactctggg tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgcgtc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccaccgccca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 2236
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2236
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro Gln
1           5           10           15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```


<210> 2237
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2237

```
atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc aaaaagctgc cgctggcgga tgttcgtgctg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tcatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
tcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acactctggg tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gctgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccaccgccca actgtatctg gcggtcaagg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2238

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2238

```
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10          15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ser	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Leu	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2240

Met	Ile	Ile	Ala	Ser	Gln	Thr	Asp	Thr	Phe	Asp	Ser	Lys	Ser	Pro	His
1				5					10					15	
Gln	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ser	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Ala	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500						505				510		
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
		530				535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2241

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2241

atgatcattg	ctagccagac	cgataccttc	gacagcaaaa	gtccgcacca	ggccagcggc	60
agcaccgtta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgcgt	120
tacggtgcga	aggttcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgtcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgca	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcgtaca	tcaccgggtgc	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttgtag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccatttg	tcgacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgcccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcttgaggca acactctggg tgatcgtttc 1320
ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gctgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcgggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2242
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2242
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1      5      10      15
Gln Ala Ser Gly Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaattttggt 480
agcatcggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgctga tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acactctgac tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcc actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 2244
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2244
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10           15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Ile Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200		205
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215		220
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230		235
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280		285
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295		300
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310		315
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345		350
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360		365
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375		380
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390		395
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	420	425		430
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440		445
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455		460
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470		475
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val	500	505		510
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520		525
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535		540
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550		555
Ser	Ser																		

<210> 2245
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2245
atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgtg ttgaaacctt cctgaacgca ggcgtgacct cgacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgctaca tcaccgggtg gctgggtggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagccggtg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggtg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgccccaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg ccacccgcca actgtatctg gcggtcaagg aagtgggtgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2246
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2246
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1 5 10 15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
50						55						60			
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70						75		80		
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115				120				125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
130			135				140								
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150		155				160				
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195				200				205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
210			215				220								
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230		235				240				
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275				280				285					
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290			295				300								
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310		315				320				
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
355			360				365								
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
370			375				380								
Ala	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390		395				400				
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420				425				430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
435			440				445								
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Arg Gln Leu Tyr Leu Ala Val					
	500		505		510
Lys Glu Val Val Gly Lys Thr Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Thr Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 2247

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2247

```

atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgt taccactggg 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgctggc caaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgca gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgca ggcgtgacct cgacgtttg cgaatttggg 480
agcatcggtg cgagcggtag cctgacccg ctggcgtaga tcaccggtag gctggttggg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtaga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgcccacat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcttgggca acactctggg tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gctgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccaccgccca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680

```

<210> 2248

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2248

```

Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10           15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195          200          205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
          210          215          220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225          230          235          240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
          245          250          255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
          260          265          270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
          275          280          285
Leu Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
          290          295          300
Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305          310          315          320
Gly Pro Ile Val Asp Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val
          325          330          335

```



```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acactctggg tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgag 1620
ctgatcgagg aggatattac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 2250
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2250

Met	Ile	Ile	Ala	Ser	Gln	Thr	Asp	Thr	Phe	Asp	Ser	Lys	Ser	Pro	Gln	1	5	10	15
Gln	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile	20	25	30	
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr	35	40	45	
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	50	55	60	
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	65	70	75	80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	85	90	95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	100	105	110	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	115	120	125	
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	130	135	140	
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170	175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val				

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ser Leu Ser Leu Gly	Ala His Ala Leu Ala	Leu Gln Gly Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His	Gln Cys Lys Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu	Glu Leu Leu Gln Gly Ser
275	280	285
Leu Leu Ile Arg Asp	Glu Leu Asp Gly Ser	His Asp Tyr Arg Gly Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg	Cys Leu Pro Gln Tyr Thr
305	310	315
Gly Pro Ile Val Asp	Gly Ile Ala Glu Ile	Ala Asn Gln Ile Glu Val
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu	Ile Asp Val Ala Gly Asn
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly	Gln Tyr Ile Gly Thr Ser
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu	Leu Ala Lys His Leu Asp
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu	Phe Asn Asn Gly Leu Pro
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Met	Val Asn Met Gly Leu Lys
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met	Pro Leu Leu Thr Phe Leu
420	425	430
Gly Asn Thr Leu Gly	Asp Arg Phe Pro Thr	His Ala Glu Gln Phe Asn
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser	Ala Asn Leu Thr Arg Gln
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala	Ile Ala Leu Met Phe Gly
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys	Ile Ala Asn His Tyr Asp
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Ala Thr Arg	Gln Leu Tyr Leu Ala Val
500	505	510
Lys Glu Val Val Gly	Lys Thr Pro Ser Lys	Asp Arg Pro Tyr Ile Trp
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His	Ile Ala Leu Ile Ala Glu
530	535	540
Asp Ile Thr Lys Asp	Gly Arg Ile Val Gln	Ala Ile Asn Gln Val Val
545	550	555
Ser Ser		

<210> 2251

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2251
atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcaaca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatgggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggc 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgtta ttgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagcctgctg atccgtgac agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctgcgcg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctggggca acactctgac tgatcgcttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcggtcaagg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2252
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2252
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro Gln
1 5 10 15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20 25 30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35 40 45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50 55 60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65 70 75 80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85 90 95

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
			420					425					430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515					520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2253
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2253

atgatcattg	ctagccagac	cgataccttc	gacagcaaaa	gtccgcacca	ggccagcgac	60
agcaccgtta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgctg	120
tatgggtgca	aggttcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tggtcgtgctg	360
ggatatgctgc	tgctgctgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggg	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgctaca	tcaccgggtg	gctggttggg	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
tcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	tcgacggtat	tgcagaaatc	gcgaatcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgctg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgtccaaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acactctggg	tgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgaccctgc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgtttggg	1440
gtgcaaagcg	ttgacctgctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	ccaccgcga	actgtatctg	gcggtcaagg	aagtgggttg	taagactccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcg	aggatatcac	taaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2254
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2254

Met	Ile	Ile	Ala	Ser	Gln	Thr	Asp	Thr	Phe	Asp	Ser	Lys	Ser	Pro	His
1				5					10					15	
Gln	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ser	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys

				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
			420					425					430				
Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465					470				475						480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545					550				555						560		
Ser	Ser																

<210> 2255

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2255

```

atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tacggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgat taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgt taccactggc 240
ttcggttggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaagctgc cgtggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggctgacctc gcacgtttg cgaatttggc 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaa tcaccgggtg gctggttggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgtggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgct ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgagcaa 840
atgctggagc tgctgcaggc cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctgggca acactctggg tgatcgtttc 1320

```

```

ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2256
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2256
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10           15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Ile Asn Ala Ser Cys Glu Trp Val
50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100         105         110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210         215         220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225         230         235         240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245         250         255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
260         265         270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
275         280         285

```

Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
290						295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425						430	
Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2257

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2257

```

atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcaaca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tacggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc gggtgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcgga tggtcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cagggtgcga gcggtatccg tctggagctg 420

```



```

attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcgggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctt ttattcacca gtgcaaaccg caccggggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgccc aaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgca taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgca 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2258
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2258
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro Gln
1           5           10           15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly

```

				165					170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225				230						235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
			245					250						255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
		260					265						270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305				310						315					320		
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
			325					330						335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
		340					345						350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
	355					360						365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370				375						380						
Ala	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385				390						395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
			405					410						415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
		420					425						430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
	435					440						445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450				455						460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly		
465				470						475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
			485					490						495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val		
		500					505						510				
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
	515					520						525					
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu		
	530				535						540						
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val		
545				550						555					560		
Ser	Ser																

<211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2259

```

atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cggatgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tacgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgtt ttgaaacctt cctgaacgcg ggctgaccc cgacgtttg cgaatttgg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaga tcaccgggtg gctggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgctggc aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgagca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttccaccgtt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccag atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatagg gcctgaaggg tctgcagatt 1260
accgtaaca gcatcatgcc gctgctgacc ttctgggca acactctggg tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gctgtttgg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2260
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2260

```

Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10          15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45

```

Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	
50						55					60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	
65					70					75					80	
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	
				85					90					95		
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	
		100					105						110			
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	
	115					120						125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	
130						135						140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	
145				150						155					160	
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	
				165					170					175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	
			180					185					190			
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	
	195						200					205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	
210						215					220					
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	
225				230						235					240	
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	
				245					250					255		
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	
			260					265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	
		275					280						285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	
290						295					300					
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	
305				310						315					320	
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	
				325					330					335		
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
			340					345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
370						375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390						395				400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
				405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
			420					425					430			
Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Leu	Phe	Gly	
465					470					475					480	

Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515				520						525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2261

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2261

atgatcattg	atagccagac	cgataccttc	gacagcaaaa	gtccgcaaca	ggccagcgac	60
agcaccgtta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgcgt	120
tacggtgcga	aggttcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcggaag	ggtgaaccga	tttacggcgt	taccactggt	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggatatgctg	tgcgtgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgcg	ggcgtgacc	cgcacgtttg	cgaatttggt	480
agcatcgggtg	cgagcgggtga	cctgaccccg	ctggcggtaca	tcaccgggtg	gctgggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagcgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtac	caaccagagc	780
ttccaccgt	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	tcgacggtat	tgcagaaatc	gcgaatcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggaacttc	1080
atggggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgccc aaat	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acactctgac	tgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaa aac	atcaacagcc	agggttttgg	cagcgcaaac	1380
ctgaccctgc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gctgtttggt	1440
gtgcaaagcg	ttgacctgcg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	ccaccgcga	actgtatctg	gcggtcaagg	aagtgggttg	taagactccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgcg	1620
ctgatcgcgg	aggatatcac	taaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2262
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2262

Met	Ile	Ile	Asp	Ser	Gln	Thr	Asp	Thr	Phe	Asp	Ser	Lys	Ser	Pro	Gln
1				5					10					15	
Gln	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
		100						105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser


```

ggcccgattg tgcacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgtttcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttcttgggca acactctggg tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg ccacccgcc actgtatctg gcggcgaagg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgctg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2264
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2264
Met Ile Ile Asp Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1      5      10      15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Ile Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240

```


Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310					315						320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325					330						335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405						410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
		420						425					430		
Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500					505					510		
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2265
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2265
 atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcacca ggccagcgac 60

```

agcaccgtta cggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcgt 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgagggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc aaaaagctgt cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaactgctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcgggc aactgcgttc atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagccagctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aacaaccgat ccaagatcgt tacagcctgc gttgcctgcc gcagtatacc 960
ggcccgattg cggacgggtat tgcggaaatc gcgaagcaaa tcgagattga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg ggtaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgtccg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctacggca acagcctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaacc atcaacagcc agggttttgg cagcgcaaac 1380
ctgaccctgc gtagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgt 1500
ctgagcccg caccctgca actgtatctg gcgattaagg aagtggttgg taaggcgccg 1560
agcaaagaac gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac cagcgggtggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt

```

<210> 2266

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2266

```

Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10           15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
        35        40        45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
        50        55        60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
        100        105        110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser

```

		115					120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150					155						160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Leu	Leu	Gly	Leu	Glu	Pro	Leu
		195				200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	His	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265						270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Gln	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Gln	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Leu	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Ala	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Lys	Gln	Ile	Glu	Ile
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Pro	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Tyr
			420					425					430		
Gly	Asn	Ser	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Arg
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly

545
Ser Ser

550

555

560

<210> 2267
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2267
atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcaaca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgct 120
cagggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg cacgggtgcga gcggtatccg tctggagctg 420
attcagcgtta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgtaaca tcaccgggtg gctgggttgg 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttgagg cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acactctggg tgatcgtttc 1320
ccgaccacg cggagcagtt caaccaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg ccacccgcca actgtatctg gcggtcaagg aagtgggtgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2268
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2268

Met	Ile	Ile	Ala	Ser	Gln	Thr	Asp	Thr	Phe	Asp	Ser	Lys	Ser	Pro	Gln
1				5					10					15	
Gln	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Gln	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135						140			
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390						395				400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		

Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435						440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
		500					505						510		
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530					535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550				555						560
Ser	Ser														

<210> 2269

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2269

```

atgattattg ctagccagac ggataaccggg gacagcaaaa gtccgcaaca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc ggttgcgaag ggtgaaccga tttacggcgt taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgcgggc caaaagctgc cgctggcggg tgttcgtgctg 360
ggatatgctg tgcgtgcgaa cagccacctg cacgggtgcg gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgca ggcgtgacct cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgctaca tcaccgggtg gctggttggg 540
ctgaacgaca gttataaccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttgag cgcgagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaaca gcatcatgcc gctgctgacc ttctgggca acactctggg tgatcgtttc 1320
ccgaccacg cgagcagtt caacaaaac atcaacagcc agggttttgg cagcgcaac 1380
ctgaccgctc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500

```

```

ctgagccccg ccacccgcca actgtatctg gcggtcaagg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

```

<210> 2270
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2270

Met	Ile	Ile	Ala	Ser	Gln	Thr	Asp	Thr	Gly	Asp	Ser	Lys	Ser	Pro	Gln	1	5	10	15
Gln	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile	20	25	30	
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr	35	40	45	
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val	50	55	60	
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly	65	70	75	80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu	85	90	95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys	100	105	110	
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser	115	120	125	
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile	130	135	140	
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170	175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185	190	
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250	255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265	270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr				

305					310					315				320	
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370				375						380				
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405					410					415		
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
		420					425						430		
Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
	435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450				455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465				470					475					480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
			485					490						495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
		500				505					510				
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
	515					520					525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
	530				535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545				550					555					560	
Ser	Ser														

<210> 2271
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2271
 atgattattg atagccagca ggataccttc gacagcaaaa gtccgcacca ggccagcgac 60
 agcaccgtta cggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
 tacggtgcca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgat taacgcgagc 180
 tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggg 240
 ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
 ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
 ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
 attcagcgta ttgaaacctt cctgaacgcg ggcgtgacct cgcacgtttg cgaatttggt 480
 agcatcggtg cgagcggtga cctgaccccg ctggcggtaca tcaccgggtg gctgggttgg 540
 ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600


```

aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccacccgt ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacgggat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcctgggca acactctgac tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgcgtc aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2272
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2272
Met Ile Ile Asp Ser Gln Gln Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10           15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20           25           30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35           40           45
Asp Lys Glu Glu Val Leu Gln Arg Ile Asn Ala Ser Cys Glu Trp Val
          50           55           60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65           70           75           80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85           90           95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145          150          155          160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165          170          175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180          185          190

```


<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2273

```
atgattattg ctagccagca ggataccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgcaggc ggttgcgaag ggtgaaccga ttacggcgtg taccactggg 240
ttcgggtggc tggcgaacgt ggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc ggggtgcgggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggg 480
agcatcggtg cgagcggtga cctgaccccg ctggcgta caaccgggtg gctgggttgg 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgctg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggta caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggc cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgccc aaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatagg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcctgggca acactctgac cgatcgtttc 1320
ccgaccacg cggagcagtt caaccaa aac atcaacagcc aggggttttg cagcgcgaac 1380
ctgaccctg aaagcattga aatcttcag caatatattg cgatcgcgct gatgtttggg 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccaccgccca actgtatctg gcggtcaagg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
```

<210> 2274

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2274

```
Met Ile Ile Ala Ser Gln Gln Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10          15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
```

65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150						155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
	195					200						205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230						235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310						315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Ala	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390						395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
465					470					475					480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from *Stanieria cyanosphaera*

<400> 2276

Met	Ile	Ile	Ala	Ser	Gln	Thr	Asp	Thr	Phe	Asp	Ser	Lys	Ser	Pro	Gln
1				5					10					15	
Gln	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Gln	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Ile	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55				60					
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265					270		
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280					285			
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360						365		
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				

Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
				405					410					415	
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420					425					430		
Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
		435					440					445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
	450					455					460				
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Leu	Phe	Gly
465					470				475						480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485					490					495	
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
			500						505				510		
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
		515					520					525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
		530				535					540				
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2277

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2277

atgatcattg	ctagccagac	cgataccttc	gacagcaaaa	gtccgcacca	ggccagcgac	60
agcaccgtta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgcgt	120
tatggtgcga	aggttcgtct	gaccgacaaa	gaggaagtgc	tgcagcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcggtggca	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcgga	tgttcgtgcg	360
ggtatgctgc	tgctgcgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgcg	ggcgtgaccc	cgcacgtttg	cgaatttggt	480
agcatcggtg	cgagcggtga	cctgaccccg	ctggcgta	tcaccgggtg	gctggttggt	540
ctgaacgaca	gttataccgt	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtaccgcgg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacggtag	caaccagagc	780
ttccaccctg	ttattcacca	gtgcaaaccg	caccgggtc	aaatttgtag	cgcgagcaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccattg	tcgacggtat	tgcagaaatc	gcgaatcaaa	tcgaggtcga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgcg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140

```

aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcttgggca acactctgac tgatcgtttc 1320
ccgacccacg cggagcagtt caaccaaacc atcaacagcc aggggttttg cagcgcgaac 1380
ctgacccgtc aaagcattga aatcttccag caatatattg cgatcgcgct gctgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcgggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2278
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2278
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1      5      10      15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
20     25     30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
35     40     45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
50     55     60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65     70     75     80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
85     90     95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
100    105    110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
115    120    125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
130    135    140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145    150    155    160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
165    170    175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
180    185    190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
195    200    205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
210    215    220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225    230    235    240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
245    250    255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro

```



```

ttcgggtggca tggcgaacgt gggttatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaaagc gggtgctgggc caaaagctgc cgctggcgga tgttcgtgcg 360
gggtatgctgc tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgag ggctgacccc cgcacgtttg cgaattttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcgtaca tcaccgggtgc gctggttggt 540
ctgaacgaca gttataacctg tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
tcgctgagcc tgggtgctga tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acactctgac tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggtttttg cagcgcgaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg ccacccgcc actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1686
agcagt

```

<210> 2280
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

```

<400> 2280
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10           15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
          100          105          110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115          120          125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130          135          140

```

Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly	145	150	155	160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly	165	170		175
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu	180	185		190
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu	195	200	205	
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val	210	215	220	
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu	225	230	235	240
Ser	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly	245	250		255
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro	260	265		270
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser	275	280	285	
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu	290	295	300	
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr	305	310	315	320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val	325	330		335
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	340	345	350	
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	355	360	365	
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	370	375	380	
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	385	390	395	400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	405	410		415
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	420	425	430	
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	435	440	445	
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	450	455	460	
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	465	470	475	480
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	485	490		495
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val	500	505	510	
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	515	520	525	
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	530	535	540	
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	545	550	555	560
Ser	Ser																		

<210> 2281
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2281
atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcaaca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgcggt 120
cagggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgat taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcgggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctgc tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgag ggctgaccc cgacgcttg cgaatttggt 480
agcatcgggtg cgagcgggtga cctgaccccg ctggcggtaca tcaccgggtgc gctgggtggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcggc tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gctgtagcc tgggtgcgca tgcgctggcg ctgcaggggc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccc caccggggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcgggc aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgagggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atggggcagc atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgcccacat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcttgggca acactctgac tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccg ccacccgcca actgtatctg gcggtcaagg aagtgggtgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686

<210> 2282
<211> 562
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2282
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro Gln
1 5 10 15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile

			20				25				30				
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Gln	Gly	Ala	Lys	Val	Arg	Leu	Thr
			35				40				45				
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Ile	Asn	Ala	Ser	Cys	Glu	Trp	Val
			50				55				60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65				70				75				80			
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
			85				90				95				
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys
			100				105				110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
			115				120				125				
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
			130				135				140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145				150				155				160			
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
			165				170				175				
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180				185				190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
			195				200				205				
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
			210				215				220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225				230				235				240			
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
			245				250				255				
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260				265				270				
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
			275				280				285				
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
			290				295				300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305				310				315				320			
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
			325				330				335				
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340				345				350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
			355				360				365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
			370				375				380				
Ala	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385				390				395				400			
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys
			405				410				415				
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
			420				425				430				

450		455		460	
Ser Ile Glu Ile Phe Gln Gln Tyr Ile Ala Ile Ala Leu Met Phe Gly					
465		470		475	480
Val Gln Ser Val Asp Leu Arg Thr Lys Lys Ile Ala Asn His Tyr Asp					
	485		490		495
Ala Ser Gln Cys Leu Ser Pro Ala Thr Arg Gln Leu Tyr Leu Ala Val					
	500		505		510
Lys Glu Val Val Gly Lys Thr Pro Ser Lys Asp Arg Pro Tyr Ile Trp					
	515		520		525
Asn Asp Asn Glu Gln Ala Leu Asp Glu His Ile Ala Leu Ile Ala Glu					
	530		535		540
Asp Ile Gly Lys Asp Gly Arg Ile Val Gln Ala Ile Asn Gln Val Val					
545		550		555	560
Ser Ser					

<210> 2283

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2283

```

atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcaaca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tatggtgcca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcaag ggtgaaccga ttacggcgt taccactggc 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgctggc caaaagctgc cgctggcgga tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgctga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgca ggcgtgacct cgacgtttg cgaatttggc 480
agcatcggtg cgagcggatga cctgaccccg ctggcgctaca tcaccgggtg gctggttggc 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtag caaccagagc 780
ttcaccctgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggctga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtgcaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggttaaca gcatcatgcc gctgctgacc ttcttgggca acactctggg tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaac atcaacagcc agggttttgg cagcggaac 1380
ctgaccctgc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggc 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccaccgccca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcac taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680

```

<210> 2284

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2284

```

Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro Gln
1      5      10      15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
      20      25      30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
      35      40      45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
      50      55      60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65      70      75      80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
      85      90      95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Gln Lys
      100     105     110
Leu Pro Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
      115     120     125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
      130     135     140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145     150     155     160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
      165     170     175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
      180     185     190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
      195     200     205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val
      210     215     220
Met Thr Gly Ile Ala Ala Asn Cys Val Tyr Asp Ala Gln Asn Leu Leu
225     230     235     240
Ala Leu Ser Leu Gly Ala His Ala Leu Ala Leu Gln Gly Leu Asn Gly
      245     250     255
Thr Asn Gln Ser Phe His Pro Phe Ile His Gln Cys Lys Pro His Pro
      260     265     270
Gly Gln Ile Trp Ser Ala Gln Gln Met Leu Glu Leu Leu Gln Gly Ser
      275     280     285
Leu Leu Ile Arg Asp Glu Leu Asp Gly Ser His Asp Tyr Arg Gly Glu
290     295     300
Asp Pro Ile Gln Asp Arg Tyr Ser Met Arg Cys Leu Pro Gln Tyr Thr
305     310     315     320
Gly Pro Ile Val Asp Gly Ile Ala Glu Ile Ala Asn Gln Ile Glu Val
      325     330     335

```

Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn	
		340						345					350			
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser	
		355					360					365				
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp	
		370				375					380					
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro	
385					390					395					400	
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys	
			405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu	
		420						425					430			
Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn	
		435					440					445				
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln	
	450					455					460					
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly	
465					470				475						480	
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp	
			485					490						495		
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val	
		500					505						510			
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp	
		515				520						525				
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu	
	530					535					540					
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val	
545					550				555						560	
Ser	Ser															

<210> 2285

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2285

```

atgattattg atagccagca ggataccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tacggtgcga aggttcgtct gaccgacaaa gaggaagtgc tgcagcgtgt taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga tttacggcgt taccactggt 240
ttcggtggca tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgt cgctggcgga tgttcgtgcg 360
ggtatgctgc tgcgtgcgaa cagccacctg cacggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgcg ggcgtgaccc cgcacgtttg cgaatttggt 480
agcatcggtg cgagcggtga cctgaccccg ctggcgtaaca tcaccggtgc gctggttggt 540
ctgaacgaca gttataccgt tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtaccgcgg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacggtac caaccagagc 780

```



```

ttccacccgt ttattcacca gtgcaaaccg caccgggtc aaatttggag cgcgcagcaa 840
atgctggagc tgctgcaggg cagcctgctg atccgtgacg agctggatgg tagccacgac 900
taccgcggcg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctctgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttaacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttcctgggca acactctggg tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaac 1380
ctgaccgctc aaagcattga aatcttccag caatatattg cgatcgcgct gatgtttggt 1440
gtgcaaagcg ttgacctgac taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcggtcaagg aagtggttgg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcgg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt
1686

```

<210> 2286

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2286

```

Met Ile Ile Asp Ser Gln Gln Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10          15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Val Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
Leu Gln Asn Asn Leu Pro Arg Tyr His Lys Ala Gly Ala Gly Lys Lys
          100         105         110
Leu Ser Leu Ala Asp Val Arg Ala Gly Met Leu Leu Arg Ala Asn Ser
          115         120         125
His Leu His Gly Ala Ser Gly Ile Arg Leu Glu Leu Ile Gln Arg Ile
          130         135         140
Glu Thr Phe Leu Asn Ala Gly Val Thr Pro His Val Cys Glu Phe Gly
145         150         155         160
Ser Ile Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala Tyr Ile Thr Gly
          165         170         175
Ala Leu Val Gly Leu Asn Asp Ser Tyr Thr Val Asp Phe Asn Gly Glu
          180         185         190
Glu Met Thr Ala Pro Glu Ala Leu Lys Arg Leu Gly Leu Glu Pro Leu
          195         200         205
Glu Leu Leu Pro Lys Glu Gly Leu Ala Met Met Asn Gly Thr Ala Val

```

210	215	220
Met Thr Gly Ile Ala	Ala Asn Cys Val Tyr Asp	Ala Gln Asn Leu Leu
225	230	235
Ala Leu Ser Leu Gly	Ala His Ala Leu Ala	Leu Gln Gly Leu Asn Gly
245	250	255
Thr Asn Gln Ser Phe	His Pro Phe Ile His	Gln Cys Lys Pro His Pro
260	265	270
Gly Gln Ile Trp Ser	Ala Gln Gln Met Leu	Glu Leu Leu Gln Gly Ser
275	280	285
Leu Leu Ile Arg Asp	Glu Leu Asp Gly Ser	His Asp Tyr Arg Gly Glu
290	295	300
Asp Pro Ile Gln Asp	Arg Tyr Ser Met Arg	Cys Leu Pro Gln Tyr Thr
305	310	315
Gly Pro Ile Val Asp	Gly Ile Ala Glu Ile	Ala Asn Gln Ile Glu Val
325	330	335
Glu Ile Asn Ser Val	Thr Asp Asn Pro Leu	Ile Asp Val Ala Gly Asn
340	345	350
Ala Ser Tyr His Gly	Gly Asn Phe Met Gly	Gln Tyr Ile Gly Thr Ser
355	360	365
Met Asp Arg Leu Arg	Tyr Tyr Leu Gly Leu	Leu Ala Lys His Leu Asp
370	375	380
Val Gln Ile Ala Leu	Leu Thr Met Pro Glu	Phe Asn Asn Gly Leu Pro
385	390	395
Ala Ser Leu Val Gly	Asn Thr Asp Arg Met	Val Asn Met Gly Leu Lys
405	410	415
Gly Leu Gln Ile Thr	Gly Asn Ser Ile Met	Pro Leu Leu Thr Phe Leu
420	425	430
Gly Asn Thr Leu Gly	Asp Arg Phe Pro Thr	His Ala Glu Gln Phe Asn
435	440	445
Gln Asn Ile Asn Ser	Gln Gly Phe Gly Ser	Ala Asn Leu Thr Arg Gln
450	455	460
Ser Ile Glu Ile Phe	Gln Gln Tyr Ile Ala	Ile Ala Leu Met Phe Gly
465	470	475
Val Gln Ser Val Asp	Leu Arg Thr Lys Lys	Ile Ala Asn His Tyr Asp
485	490	495
Ala Ser Gln Cys Leu	Ser Pro Ala Thr Arg	Gln Leu Tyr Leu Ala Val
500	505	510
Lys Glu Val Val Gly	Lys Thr Pro Ser Lys	Asp Arg Pro Tyr Ile Trp
515	520	525
Asn Asp Asn Glu Gln	Ala Leu Asp Glu His	Ile Ala Leu Ile Ala Glu
530	535	540
Asp Ile Gly Lys Asp	Gly Arg Ile Val Gln	Ala Ile Asn Gln Val Val
545	550	555
Ser Ser		

<210> 2287

<211> 1686

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2287

```
atgatcattg ctagccagac cgataccttc gacagcaaaa gtccgcacca ggccagcgac 60
agcaccgtta cgggtgggtga taagccgctg acgatcaatg aggtgtcggc tgttgcgctg 120
tacgggtgca aggttcgtct gaccgacaaa gaggaagtgc tgcagcgat taacgcgagc 180
tgcgagtggg tggcgaggc gggtgcgaag ggtgaaccga ttacggcgt taccactgg 240
ttcgggtggc tggcgaacgt gggtatcacc ccggaccagg cgaaggagct gcagaataac 300
ctgccacgct atcacaagc gggtgcgggc aaaaagctgc cgctggcggg tgttcgtgcg 360
ggatatgctg tgcgtgcgaa cagccacctg caggtgcga gcggtatccg tctggagctg 420
attcagcgta ttgaaacctt cctgaacgca ggctgacct cgacgtttg cgaatttggt 480
agcatcgggt cgagcgggtga cctgaccccg ctggcgatca tcaccgggtg gctggttggt 540
ctgaacgaca gttataacct tgattttaac ggcgaggaaa tgaccgcgcc ggaggcgctg 600
aaacgcctgg gtctggagcc gctggaactg ctgccgaagg aaggcctggc gatgatgaac 660
ggtagcgcg tgatgaccgg tattgcggcg aactgcgttt atgatgcgca gaacctgctg 720
gcgctgagcc tgggtgcgca tgcgctggcg ctgcagggcc tgaacgggtac caaccagagc 780
ttccaccctg ttattcacca gtgcaaaccg caccgggtc aaatttgagg cgcgagcaa 840
atgctggagc tgctgcaggc cagcctgctg atccgtgac agctggatgg tagccacgac 900
taccgcgccg aagatccgat ccaagatcgt tacagcatgc gttgcctgcc gcagtatacc 960
ggcccgattg tcgacggtat tgcagaaatc gcgaatcaaa tcgaggtcga aatcaacagc 1020
gtgaccgaca acccgctgat cgatgttgcg gggaacgcga gctaccacgg tggcaacttc 1080
atgggcccagt atattggtac cagcatggac cgtctgcgtt actatctggg cctgctggcg 1140
aaacacctgg atgtccaaat cgcgctgctg accatgccgg agtttaacaa cggctcgccg 1200
gctagcctgg tgggtaacac cgaccgcatg gttacatgg gcctgaaggg tctgcagatt 1260
accggtaca gcatcatgcc gctgctgacc ttctgggca acactctgac tgatcgtttc 1320
ccgaccacg cggagcagtt caacaaaaac atcaacagcc agggttttgg cagcgcgaa 1380
ctgaccctg aaagcattga aatcttcag caatatatt cgatcgcgct gctgtttggt 1440
gtgcaaagcg ttgacctgcg taccaagaaa attgcgaacc actacgatgc gagccaatgc 1500
ctgagcccgg ccacccgcca actgtatctg gcggtcaagg aagtgggttg taagactccg 1560
agcaaagatc gtccgtatat ctggaacgac aacgagcagg cgctggatga acacattgcg 1620
ctgatcgcg aggatatcgg taaagatggc cgtattgttc aggcgatcaa ccaagtgggt 1680
agcagt 1686
```

<210> 2288

<211> 562

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2288

```
Met Ile Ile Ala Ser Gln Thr Asp Thr Phe Asp Ser Lys Ser Pro His
1           5           10          15
Gln Ala Ser Asp Ser Thr Val Thr Val Gly Asp Lys Pro Leu Thr Ile
          20          25          30
Asn Glu Val Ser Ala Val Ala Arg Tyr Gly Ala Lys Val Arg Leu Thr
          35          40          45
Asp Lys Glu Glu Val Leu Gln Arg Ile Asn Ala Ser Cys Glu Trp Val
          50          55          60
Ala Gln Ala Val Ala Lys Gly Glu Pro Ile Tyr Gly Val Thr Thr Gly
65          70          75          80
Phe Gly Gly Met Ala Asn Val Val Ile Thr Pro Asp Gln Ala Lys Glu
          85          90          95
```

Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Lys	Lys		
			100					105					110				
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser		
		115					120					125					
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile		
	130					135					140						
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly		
145					150					155					160		
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly		
				165					170						175		
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu		
			180					185					190				
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu		
		195					200					205					
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val		
	210					215					220						
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu		
225					230					235					240		
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly		
				245					250					255			
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro		
			260					265						270			
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser		
		275					280					285					
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu		
	290					295					300						
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr		
305					310					315					320		
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val		
				325					330					335			
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn		
			340					345					350				
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser		
		355					360					365					
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp		
	370					375					380						
Val	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro		
385					390					395					400		
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys		
				405					410					415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu		
			420					425					430				
Gly	Asn	Thr	Leu	Thr	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn		
		435					440					445					
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln		
	450					455					460						
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Leu	Phe	Gly		
465					470					475					480		
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp		
				485					490					495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val		
			500					505					510				
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp		
		515					520					525					

Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
530						535					540				
Asp	Ile	Gly	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
545					550					555					560
Ser	Ser														

<210> 2289
 <211> 1686
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2289

atgatcattg	ctagccagac	cgataccttc	gacagcaaaa	gtccgcacca	ggccagcgac	60
agcaccgtta	cggtgggtga	taagccgctg	acgatcaatg	aggtgtcggc	tgttgcgctg	120
tacgggtgca	aggttcgtct	gaccgacaaa	gaggaagtgc	tgacgcgtgt	taacgcgagc	180
tgcgagtggg	tggcgcaggc	ggttgcgaag	ggtgaaccga	tttacggcgt	taccactggg	240
ttcgggtggc	tggcgaacgt	ggttatcacc	ccggaccagg	cgaaggagct	gcagaataac	300
ctgccacgct	atcacaaagc	gggtgcgggc	caaaagctgc	cgctggcggg	tggtcgtgctg	360
ggatatgctgc	tgctgctgaa	cagccacctg	cacggtgcga	gcggtatccg	tctggagctg	420
attcagcgta	ttgaaacctt	cctgaacgcg	ggcgtgacct	cgacgctttg	cgaatttggt	480
agcatcggtg	cgagcgggtg	cctgaccccg	ctggcgctaca	tcaccgggtg	gctgggttgg	540
ctgaacgaca	gttataacct	tgattttaac	ggcgaggaaa	tgaccgcgcc	ggaggcgctg	600
aaacgcctgg	gtctggagcc	gctggaactg	ctgccgaagg	aaggcctggc	gatgatgaac	660
ggtagccgcg	tgatgaccgg	tattgcggcg	aactgcgttt	atgatgcgca	gaacctgctg	720
gcgctgagcc	tgggtgcgca	tgcgctggcg	ctgcagggcc	tgaacgggtg	caaccagagc	780
ttccacccgt	ttattcacca	gtgcaaaccg	caccgggtgc	aaatttggag	cgcgagcaaa	840
atgctggagc	tgctgcaggg	cagcctgctg	atccgtgacg	agctggatgg	tagccacgac	900
taccgcggcg	aagatccgat	ccaagatcgt	tacagcatgc	gttgccctgcc	gcagtatacc	960
ggcccgattg	tcgacggtat	tgcagaaatc	gcgaatcaaa	tcgaggctga	aatcaacagc	1020
gtgaccgaca	acccgctgat	cgatgttgctg	gggaacgcga	gctaccacgg	tggcaacttc	1080
atgggcccagt	atattggtac	cagcatggac	cgtctgcgtt	actatctggg	cctgctggcg	1140
aaacacctgg	atgcccacaa	cgcgctgctg	accatgccgg	agtttaacaa	cggtctgccg	1200
gctagcctgg	tgggtaacac	cgaccgcatg	gttaacatgg	gcctgaaggg	tctgcagatt	1260
accggtaaca	gcatcatgcc	gctgctgacc	ttcctgggca	acactctggg	tgatcgtttc	1320
ccgaccacg	cggagcagtt	caaccaaacc	atcaacagcc	agggttttgg	cagcgcgaa	1380
ctgacccgtc	aaagcattga	aatcttccag	caatatattg	cgatcgcgct	gatgttttgg	1440
gtgcaaagcg	ttgacctgctg	taccaagaaa	attgcgaacc	actacgatgc	gagccaatgc	1500
ctgagcccgg	ccacccgcc	actgtatctg	gcggtcaagg	aagtgggttg	taagactccg	1560
agcaaagatc	gtccgtatat	ctggaacgac	aacgagcagg	cgctggatga	acacattgctg	1620
ctgatcgcg	aggatatcac	taaagatggc	cgtattgttc	aggcgatcaa	ccaagtgggt	1680
agcagt						1686

<210> 2290
 <211> 562
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Tyrosine Ammonia Lyase from Stanieria cyanosphaera

<400> 2290

Met	Ile	Ile	Ala	Ser	Gln	Thr	Asp	Thr	Phe	Asp	Ser	Lys	Ser	Pro	His
1				5					10					15	
Gln	Ala	Ser	Asp	Ser	Thr	Val	Thr	Val	Gly	Asp	Lys	Pro	Leu	Thr	Ile
			20					25					30		
Asn	Glu	Val	Ser	Ala	Val	Ala	Arg	Tyr	Gly	Ala	Lys	Val	Arg	Leu	Thr
		35					40					45			
Asp	Lys	Glu	Glu	Val	Leu	Gln	Arg	Val	Asn	Ala	Ser	Cys	Glu	Trp	Val
	50					55					60				
Ala	Gln	Ala	Val	Ala	Lys	Gly	Glu	Pro	Ile	Tyr	Gly	Val	Thr	Thr	Gly
65					70					75					80
Phe	Gly	Gly	Met	Ala	Asn	Val	Val	Ile	Thr	Pro	Asp	Gln	Ala	Lys	Glu
				85					90					95	
Leu	Gln	Asn	Asn	Leu	Pro	Arg	Tyr	His	Lys	Ala	Gly	Ala	Gly	Gln	Lys
			100					105					110		
Leu	Pro	Leu	Ala	Asp	Val	Arg	Ala	Gly	Met	Leu	Leu	Arg	Ala	Asn	Ser
		115					120					125			
His	Leu	His	Gly	Ala	Ser	Gly	Ile	Arg	Leu	Glu	Leu	Ile	Gln	Arg	Ile
	130					135					140				
Glu	Thr	Phe	Leu	Asn	Ala	Gly	Val	Thr	Pro	His	Val	Cys	Glu	Phe	Gly
145					150					155					160
Ser	Ile	Gly	Ala	Ser	Gly	Asp	Leu	Thr	Pro	Leu	Ala	Tyr	Ile	Thr	Gly
				165					170					175	
Ala	Leu	Val	Gly	Leu	Asn	Asp	Ser	Tyr	Thr	Val	Asp	Phe	Asn	Gly	Glu
			180					185					190		
Glu	Met	Thr	Ala	Pro	Glu	Ala	Leu	Lys	Arg	Leu	Gly	Leu	Glu	Pro	Leu
		195					200					205			
Glu	Leu	Leu	Pro	Lys	Glu	Gly	Leu	Ala	Met	Met	Asn	Gly	Thr	Ala	Val
	210					215					220				
Met	Thr	Gly	Ile	Ala	Ala	Asn	Cys	Val	Tyr	Asp	Ala	Gln	Asn	Leu	Leu
225					230					235					240
Ala	Leu	Ser	Leu	Gly	Ala	His	Ala	Leu	Ala	Leu	Gln	Gly	Leu	Asn	Gly
				245					250					255	
Thr	Asn	Gln	Ser	Phe	His	Pro	Phe	Ile	His	Gln	Cys	Lys	Pro	His	Pro
			260					265						270	
Gly	Gln	Ile	Trp	Ser	Ala	Gln	Gln	Met	Leu	Glu	Leu	Leu	Gln	Gly	Ser
		275					280						285		
Leu	Leu	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Ser	His	Asp	Tyr	Arg	Gly	Glu
	290					295					300				
Asp	Pro	Ile	Gln	Asp	Arg	Tyr	Ser	Met	Arg	Cys	Leu	Pro	Gln	Tyr	Thr
305					310					315					320
Gly	Pro	Ile	Val	Asp	Gly	Ile	Ala	Glu	Ile	Ala	Asn	Gln	Ile	Glu	Val
				325					330					335	
Glu	Ile	Asn	Ser	Val	Thr	Asp	Asn	Pro	Leu	Ile	Asp	Val	Ala	Gly	Asn
			340					345					350		
Ala	Ser	Tyr	His	Gly	Gly	Asn	Phe	Met	Gly	Gln	Tyr	Ile	Gly	Thr	Ser
		355					360					365			
Met	Asp	Arg	Leu	Arg	Tyr	Tyr	Leu	Gly	Leu	Leu	Ala	Lys	His	Leu	Asp
	370					375					380				
Ala	Gln	Ile	Ala	Leu	Leu	Thr	Met	Pro	Glu	Phe	Asn	Asn	Gly	Leu	Pro
385					390					395					400
Ala	Ser	Leu	Val	Gly	Asn	Thr	Asp	Arg	Met	Val	Asn	Met	Gly	Leu	Lys

				405				410				415			
Gly	Leu	Gln	Ile	Thr	Gly	Asn	Ser	Ile	Met	Pro	Leu	Leu	Thr	Phe	Leu
				420				425				430			
Gly	Asn	Thr	Leu	Gly	Asp	Arg	Phe	Pro	Thr	His	Ala	Glu	Gln	Phe	Asn
				435				440				445			
Gln	Asn	Ile	Asn	Ser	Gln	Gly	Phe	Gly	Ser	Ala	Asn	Leu	Thr	Arg	Gln
				450				455				460			
Ser	Ile	Glu	Ile	Phe	Gln	Gln	Tyr	Ile	Ala	Ile	Ala	Leu	Met	Phe	Gly
				465				470				475			
Val	Gln	Ser	Val	Asp	Leu	Arg	Thr	Lys	Lys	Ile	Ala	Asn	His	Tyr	Asp
				485				490				495			
Ala	Ser	Gln	Cys	Leu	Ser	Pro	Ala	Thr	Arg	Gln	Leu	Tyr	Leu	Ala	Val
				500				505				510			
Lys	Glu	Val	Val	Gly	Lys	Thr	Pro	Ser	Lys	Asp	Arg	Pro	Tyr	Ile	Trp
				515				520				525			
Asn	Asp	Asn	Glu	Gln	Ala	Leu	Asp	Glu	His	Ile	Ala	Leu	Ile	Ala	Glu
				530				535				540			
Asp	Ile	Thr	Lys	Asp	Gly	Arg	Ile	Val	Gln	Ala	Ile	Asn	Gln	Val	Val
				545				550				555			
Ser	Ser														